

GenCore version 5.1.6
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leic search, using sw model

April 21, 2004, 06:00:54 ; Search time 15317 Seconds
(without alignments)
11437.784 Million cell updates/sec

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470272 seqs, 21671516995 residues

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Minimum Match 0%
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Listing first 45 summaries

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s the number of results predicted by chance to have a

score greater than or equal to the score of the result being f
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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LOCUS AX001446 4042 bp
DEFINITION Sequence 1 from Patent WO9859040.
ACCESSION AX001446
VERSION AX001446.1 GI:7241612
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick,M. and Hagen,G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AN
THERAPEUTIC USE
JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;


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yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

M. and Hagen,G.
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t: WO 9933998-A 2 08-JUL-1999;
MARESA (DE); BAYER AG (DE)
Location/Qualifiers
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100.0%; Score 4042; DB 6; Length 4042;
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4037)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase
drug screening
JOURNAL Patent: US 6617110-A 343 09-SEP-2003;
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AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,
Harley,C.B. and Andrews,W.H.
TITLE
Human telomerase catalytic subunit
JOURNAL
Patent: EP 133094-A 343 06-AUG-2003;
Geron Corporation (US); University Technology Corporati-
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VERSION BD011070.1 GI:18639443
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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4037)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,C
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 27 27-MAR-2001;
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FH Key Location/Qualifiers

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;C.J., Kipling,D.G., Wilkinson,G., Mcsharry,B.D. and
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QY	3668	GAGTGTCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCC
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QY	3788	CCAGATTCGCATTTTCAACCCCTCGCCCTGCCCCTCTTTGGCTTCCACCCCA
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RESULT 11

11:43:34 2004

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QY	3068	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCAACGCATGTGTCTGCAGCTCCC
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11:43:34 2004

us-09-424-686f-1.rge

[illegible]

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QY	2768	GACAGTGGTGAACTTCCCTGTAGAACGAGGCCCTGGGTGGCACGGCTTTTGT
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Db	3061	CAAGATCCTCTCTGCTGCAGCGGTACAGGTTTACGCATGTGTGCTGCAGCTCCC
QY	3128	TCAGCAAGTTTGGAGAAACCCACATTTTCTCGCGGTCACTCTGACACGGC
Db	3121	TCAGCAAGTTTGGAGAAACCCACATTTTCTCGCGGTCACTCTGACACGGC
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QY	3488	GAGCAGACACCGAGGCCCTGTTCAGCCGGGCTCTACGTCCCAGGGAGGGAGGGG
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11:43:34 2004

us-09-424-686f-1.rge

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QY	2468	CAGTGGCCCTCTTCGACGCTCTTCCACGCTTCATGTGCACCAACGCGCGTGC
DB	2461	CAGTGGCCCTCTTCGACGCTCTTCCACGCTTCATGTGCACCAACGCGCGTGC
QY	2528	CAAGTCCCTACGTCACGTCAGGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCT
DB	2521	CAAGTCCCTACGTCAGTCAGGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCT
QY	2588	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGCGGGGATTCGGCGGGA
DB	2581	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGCGGGGATTCGGCGGGA
QY	2648	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGC
DB	2641	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCCACGC
QY	2708	CTTCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTT
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QY	2828	GCCGGCCACGGCCCTATTCCCTGGTGGTGGCCCTGCTGTGGATACCCGGACCCCT
DB	2821	GCCGGCCACGGCCCTATTCCCTGGTGGTGGCCCTGCTGTGGATACCCGGACCCCT
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April 21, 2004, 21:01:01
secs

GenCore version 5.1.6
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eic search, using sw model

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(without alignments)
11916.181 Million cell updates/sec

S-09-424-686F-1
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373863 seqs, 2124099041 residues
its satisfying chosen parameters: 6747726

ngth: 0
ngth: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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: Geneseqn2000s: *
: Geneseqn2001as: *
: Geneseqn2001bs: *
: Geneseqn2002s: *
: Geneseqn2003as: *
: Geneseqn2003bs: *
: Geneseqn2003cs: *
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s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

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99.6	4037	2	AAV22428			Aav22428 Human tel
99.5	4023	2	AAV60320			Aav60320 Human tel
99.3	4070	6	ABL53711			Ab153711 Human tel
99.3	4015	2	AAZ00724			Aaz00724 Human tel
99.3	4015	2	AAZ20279			Aaz20279 Human tel
99.3	4015	2	AAZ30154			Aaz30154 CDNA enco
99.3	4015	4	AAH45901			Aah45901 Human hTE
99.3	4015	6	AAH46821			Aad46821 Human tel
99.3	4015	6	ABA97534			Aba97534 Cancer ce
99.3	4015	7	ACC58039			Acc58039 Human tel
99.3	4015	7	ACC57552			Acc57552 Human tel
99.3	4015	7	ABZ22474			Abz22474 Human tel
99.3	4015	7	ACC44482			Acc44482 Human tel
99.3	4015	2	AAZ08150			Aaz08150 Human tel
99.3	4015	7	ABZ18391			Abz18391 Group III
99.3	4027	2	AAH89424			Aax89424 Human EST
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39	3278.8	81.1	3500	2	AAH18275	Aax18275
40	3201.4	79.2	3203	2	AAH18268	Aax18268
41	3121	77.2	3167	2	AAH18271	Aax18271
42	3121	77.2	3167	2	AAH18280	Aax18280
43	3077.4	76.1	7688	2	AAH18351	Aax18351
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45	2889.2	71.5	7797	2	AAH18350	Aax18350

ALIGNMENTS

RESULT 1
AAV72117
ID AAV72117 standard; cDNA; 4042 BP.
XX AC AAV72117;
XX DT 24-MAY-1999 (first entry)
XX DE Human catalytic telomerase sub-unit cDNA.
XX KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; as
KW modulator; treatment; inhibit; cellular disorder; death; defect;
KW ageing; antisense; neoplastic cell; telomerase-related condition;
KW tumour cell; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 63..3461
FT /*tag= a
FT /product= "catalytic telomerase subunit"
XX PN WO9859040-A2.
XX PD 30-DEC-1998.
XX PF 09-JUN-1998; 98WO-EP003468.
XX PR 20-JUN-1997; 97DE-01026329.
XX PR 26-MAR-1998; 98DE-01013274.
XX PR 14-APR-1998; 98DE-01016496.
XX PA (FARB) BAYER AG.
XX PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX DR WPI; 1999-081276/07.
XX DR P-PSDB; AAW90251.
XX PT New catalytically active subunit of human telomerase - used in t
PT modulation of telomerase activity, particularly for treating can
PT ageing.
XX PS Claim 4; Fig 1; 76pp; German.
XX CC This sequence encodes a novel human catalytic telomerase sub-unit

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us-09-424-686f-1.rng

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QY	3001	TGAAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGT
Db	3001	TGAAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGT
QY	3061	ACATCTACAAGATCCTCTGTCTGCAGGCGTACAGGTTTCAACGCATGTGTGCTGT
Db	3061	ACATCTACAAGATCCTCTGTCTGCAGGCGTACAGGTTTCAACGCATGTGTGCTGT
QY	3121	CATTTTCATCAGCAAGTTTGGAAAGAACCCCAACATTTTTCTCGCGGTCACTCTCTGT
Db	3121	CATTTTCATCAGCAAGTTTGGAAAGAACCCCAACATTTTTCTCGCGGTCACTCTCTGT
QY	3181	CCTCCCTCTGTACTCCATCCTGTAAAGCAAGCAAGACGCAGGGATGTGCTGGGG
Db	3181	CCTCCCTCTGTACTCCATCCTGTAAAGCAAGCAAGACGCAGGGATGTGCTGGGG
QY	3241	GGCCCGCGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCAT
Db	3241	GGCCCGCGGCGCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCAT
QY	3301	TCAAGCTGACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGAC
Db	3301	TCAAGCTGACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGAC
QY	3361	AGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGTGACTGCCCTGGAGGCCG
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QY	3421	ACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCF
Db	3421	ACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCF
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QY	3541	GGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGT
Db	3541	GGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGT
QY	3601	AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGT
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QY	3661	AAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCT
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Db	3841	ACCATCCAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTG
QY	3901	AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGG
Db	3901	AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGG
QY	3961	TTGGGGGAGGTGCTGTGGGAGTAAAAATACTGAATATATAGATTTTTTTCAGTTTTG
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standard; cDNA; 4023 BP.

(first entry)

erase gene referred to as hEST2.

ubunit; human; telomerase; telomere maintenance; diagnosis;
cancer; ss.

OS	Homo sapiens.
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FH	Key Location/Qualifiers
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FT	/tag= a
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PN	WO9837181-A2.
XX	
PD	27-AUG-1998.
XX	
PF	20-FEB-1998; 98WO-US003404.
XX	
PR	20-FEB-1997; 97US-0038750P.
PR	20-MAY-1997; 97US-0047151P.
PR	01-AUG-1997; 97US-0054549P.
PR	14-AUG-1997; 97US-0055762P.
PR	30-OCT-1997; 97US-0064322P.
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.
XX	
PI	Counter CM, Meyerson M, Weinberg RA;
XX	
DR	WPI; 1998-495367/42.
DR	P-PSDB; AAW71376.
XX	
PT	New isolated human telomerase catalytic sub-unit gene - used to
PT	products for increasing or reducing the life span of cells such
PT	cells or transformed cells.
XX	
PS	Claim 5; Fig 5A-B; 96pp; English.
XX	
CC	The present sequence encodes the catalytic subunit of a human t,
CC	holoenzyme. Disruption of the telomerase gene alters telomere
CC	maintenance. The DNA is essential for telomerase activity, and i
CC	protein is physically associated with telomerase and a constitut
CC	active telomerase complex. The products can be used for increas
CC	reducing the lifespan of cells such as cancer cells or transform
CC	They can also be used in the diagnosis and treatment of malignan
CC	addition, cells with a longer lifespan can be transplanted into
CC	grafted onto an individual (e.g. as skin grafts, as systems for
CC	of therapeutic proteins, such as hormones and enzymes), to whom
CC	provide therapeutic benefit
XX	
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	Query Match 99.5%; Score 4019.8; DB 2; Length 4023;
	Best Local Similarity 100.0%; Pred.No. 0;
	Matches 4021; Conservative 0; Mismatches 2; Indels 0;
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Dd	
	1 CAGGCAGCGTGGCTGCTGTGTCGCCACGTGGGAAGCCCTGGCCCCCGGCACCCC
QY	65 GCCCGCGCTCCCCGCTGCCGAGCCGTGGCGCTCCCTGTGCGCAGCCACTACCG
Dd	
	61 GCCCGCGCTCCCCGCTGCCGAGCCGTGGCGCTCCCTGTGCGCAGCCACTACCG
QY	125 GCTGCCGTGGCCACGTTTCGTGCGGGCGCTGGGGCCCCAGGGCTGGCGTGCTG
Dd	
	121 GCTGCCGTGGCCACGTTTCGTGCGGGCGCTGGGGCCCCAGGGCTGGCGTGCTG
QY	185 CGGGGACCCGGCGGCTTTCGGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTGCCC
Dd	
	181 CGGGGACCCGGCGGCTTTCGGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTGCCC
QY	245 CGCACGGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGTCTGCTGAAGGAC
Dd	
	241 CGCACGGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGTCTGCTGAAGGAC
QY	305 GGCCCCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCCTTC
Dd	
	301 GGCCCCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCCTTC

11:43:35 2004

us-09-424-686f-1.rng

GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCAGGCCCTTCACCACGAGCGTGCGCAG	424
GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCAGGCCCTTCACCACGAGCGTGCGCAG	420
CCTGCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGCTGCT	484
CCTGCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGCTGTT	480
CCGCGTGGGCGACGACGTGCTGTTTCACTTGCTGGCACTGCGCGCTCTTTTGCT	544
CCGCGTGGGCGACGACGTGCTGTTTCACTTGCTGGCACTGCGCGCTCTTTTGCT	540
GGCTCCCAAGCTGGCCCTACCAAGGTGTGCGGGCCGCGCTGTACCACTCGGGCGTGC	604
GGCTCCCAAGCTGGCCCTACCAAGGTGTGCGGGCCGCGCTGTACCACTCGGGCGTGC	600
TCAGGCCCGGCCCGCCACACGCTAGTGGAACCCGAAGCGCTTGGGATGCGAAG	664
TCAGGCCCGGCCCGCCACACGCTAGTGGAACCCGAAGCGCTTGGGATGCGAAG	660
CTGGAACCATAGCGTCAGGAGGCCGGGTCCCCTGCGCTGCCAGCCCCGGGTGC	724
CTGGAACCATAGCGTCAGGAGGCCGGGTCCCCTGCGCTGCCAGCCCCGGGTGC	720
GAGGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCCAAGCGCTGG	784
GAGGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCCAAGCGCTGG	780
TGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTTGGGCCACCCCGGGCAG	844
TGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTTGGGCCACCCCGGGCAG	840
GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGA	904
GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGA	900
CACCTCTTTGGAGGGTGCGTCTCTTGGCACGGGCCACTCCACCCATCCGTGGGCGG	964
CACCTCTTTGGAGGGTGCGTCTCTTGGCACGGGCCACTCCACCCATCCGTGGGCGG	960
GCACACGGGGCCCCCATCCACATCGCGGCACCACTCCCTGGGACACGCCCTTG	1024
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CCCGGTGTACGCCGAGACCAAGCACTTCTACTCTCTCAGGCGACAAGGAGCAGCT	1084
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GCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGT	1144
GCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGT	1140
GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGG	1204
GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGG	1200
GCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAAGC	1264
GCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAAGC	1260
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GTGCCCTACGGGTGCTCCTCAAGACGCACCTGCCCCGTGCGAGCTGCGGTACCCC	1320
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AGCCGGTGCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGA	1380
CACAGACCCCGCTGCGCTGGTGACGTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGT	1444
CACAGACCCCGCTGCGCTGGTGACGTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGT	1440
CGGCTTCGTGCGGGCCCTGCTGCGCGGGTGTGTTGTCCTCCAGGCCCTCTGGGGCTCCAG	1504

Db	1441	 GTACGGCTTCGTGCGGCTGCCTGCGCGGCTGGTGCCCCCAGGCCCTCTGGGG
QY	1505	GCACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAA
Db	1501	GCACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAA
QY	1565	CAAGCTCTCGCTCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTG
Db	1561	CAAGCTCTCGCTCAGGAGCTGACGTGGAAGATGAGCGTGCGGGCTGCGCTTG
QY	1625	CAGGAGCCCAGGGGTGGCTGTGTTCGGCCGCGAGACACCGTCTGCGTGAGGA
Db	1621	CAGGAGCCCAGGGGTGGCTGTGTTCGGCCGCGAGACACCGTCTGCGTGAGGA
QY	1685	GGCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTC
Db	1681	GGCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTC
QY	1745	TTATGTACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCCGGAAGAGT
Db	1741	TTATGTACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCCGGAAGAGT
QY	1805	GAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGC
Db	1801	GAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGC
QY	1865	GTCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTC
Db	1861	GTCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTC
QY	1925	CCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTC
Db	1921	CCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTC
QY	1985	AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAG
Db	1981	AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAG
QY	2045	GTTCAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCT
Db	2041	GTTCAGCGTGTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCT
QY	2105	GGGCTTGGACGATATCCACAGGGCCTTGGGCGACCTTCGTGCTGCTGCGGGCC
Db	2101	GGGCTTGGACGATATCCACAGGGCCTTGGGCGACCTTCGTGCTGCTGCGGGCC
QY	2165	CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACC
Db	2161	CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACC
QY	2225	CCAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAACCCAGAAACAGTAC
Db	2221	CCAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAACCCAGAAACAGTAC
QY	2285	GGTCCGTTATGCCGTGGTCCAGAAAGGCGGCCCATGGGCAAGTCCGCAAGGCCCTTC
Db	2281	GGTCCGTTATGCCGTGGTCCAGAAAGGCGGCCCATGGGCAAGTCCGCAAGGCCCTTC
QY	2345	CCACGTCTTACCTTGACAGACCTCCAGCCGTACATCGGACAGTTCTGTTGGCTCAC
Db	2341	CCACGTCTTACCTTGACAGACCTCCAGCCGTACATCGGACAGTTCTGTTGGCTCAC
QY	2405	GGAGACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCCCTGAAT
Db	2401	GGAGACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCCCTGAAT
QY	2465	CAGCAGTGGCCTCTTCGACGCTTCTCTACGCTTTCATGTGCCACACGCCGTGCGC
Db	2461	CAGCAGTGGCCTCTTCGACGCTTCTCTACGCTTTCATGTGCCACACGCCGTGCGC
QY	2525	GGGCAAGTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCTCCACG

3CAAGTCCTACGTCCAGTCCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCT 2580
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3CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGGACGG 2640
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CCTTCTCAGGACCCCTGTCGGAGGTGTCCCTGAGTATGGCTGCGTGGTGAATTCGG 2760
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AGACAGTGGTGAACTTCCCTGTAGAGACGAGGCCCTGGTGGCACGGCTTTGTTCA 2820
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TGCCGGCCCCACGGCCTATTCCCTGTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2880
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTTCATCAGAGCCAGTCTCACCTTCAA 2944
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTTCATCAGAGCCAGTCTCACCTTCAA 2940
3CGGCTTCAAGGCTGGAGGAAATGCGTTCGCAAACTTTTGGGGTCTTGGGCTGAA 3004
3CGGCTTCAAGGCTGGAGGAAATGCGTTCGCAAACTTTTGGGGTCTTGGGCTGAA 3000
3TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCTCCAGACGGTGTGACCAACAT 3064
3TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCTCCAGACGGTGTGACCAACAT 3060
ACAAGATCCTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGAGTCCCAT 3124
ACAAGATCCTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGAGTCCCAT 3120
ATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTCACTCTGACAGCGCCTC 3184
ATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGCGTCACTCTGACAGCGCCTC 3180
TCTGTACTCCATCCTGAAAGCCAAAGAACGAGGATGTCGTGGGGCCAAAGGGCGC 3244
TCTGTACTCCATCCTGAAAGCCAAAGAACGAGGATGTCGTGGGGCCAAAGGGCGC 3240
TGGCCCTCTGCCCCTCGAGGCGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3304
TGGCCCTCTGCCCCTCGAGGCGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
TGACTCGACACCGGTGCTACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3364
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TGACTCGAGTGGAGTCCCGGGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
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TACTGCCCTCAGACTTCAAGACCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
TAGCAGACACACGAGCCCTGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3544
TAGCAGACACACGAGCCCTGTCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
TACACCCAGGCGCGACCTGCTGGAGTCTGAGGCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 3604
TACACCCAGGCGCGACCTGCTGGAGTCTGAGGCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 3600
TATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3664
TATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3660

QY 3665 GCTGAGTGTCCAGACACCTGCGCTTCTCACTTCCCCACAGGCTGGCGTCCGC
Db 3661 GCTGAGTGTCCAGACACCTGCGCTTCTCACTTCCCCACAGGCTGGCGTCCGC
QY 3725 CCAGGGCCAGCTTTTCTTCCCTCACAGGAGCCCGCTTCCACTCCCCACATAGGAAT
Db 3721 CCAGGGCCAGCTTTTCTTCCCTCACAGGAGCCCGCTTCCACTCCCCACATAGGAAT
QY 3785 TCCCCAGATTGCGCATTTGTTTCAACCCCTCGCCCTGCGCTTCTTGTGCTTCCACCC
Db 3781 TCCCCAGATTGCGCATTTGTTTCAACCCCTCGCCCTGCGCTTCTTGTGCTTCCACCC
QY 3845 TCCAGGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACC
Db 3841 TCCAGGTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACC
QY 3905 GTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCA
Db 3901 GTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCA
QY 3965 GGGGAGGTGCTGTTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAA
Db 3961 GGGGAGGTGCTGTTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAA
QY 4025 AAA 4027
Db 4021 AAA 4023

RESULT 4

ABL53711
ID ABL53711 standard; cDNA; 4070 BP.

XX ABL53711;

DT 17-JUN-2002 (first entry)

XX Human telomerase catalytic subunit hTERT cDNA.

DE hTERT; telomerase; reverse transcriptase; immortalisation; human
vaccine; enzyme; gene; ss.

OS Homo sapiens.

XX WO200216555-A2.

PN 28-FEB-2002.

XX 17-AUG-2001; 2001WO-GB003726.

XX 17-AUG-2000; 2000GB-00020246.

PR 17-AUG-2000; 2000US-0225734P.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

PA Jones CJ, Kipling DG, Wilkinson G, Mcsharry B, Skinner JW;
WPI; 2002-315462/35.

DR Novel hTERT-immortalized cell line (human telomerase reverse
transcriptase) useful for human vaccine production and preparat;
antigen, such as a virus or virus-derived agent.

XX Example 1; Fig 1; 64pp; English.

CC The present sequence is that of hTERT cDNA in plasmid pGRN121.1
the catalytic subunit of human telomerase. Claimed immortalised
lines for use in vaccine production are adapted to express hTERT
Suitable cell lines comprise human diploid fibroblasts, e.g. MRC
WI38 cells, transfected with hTERT cDNA or infected by a retrovi
carrying hTERT cDNA, and are capable of supporting antigen produ
method for preparing such cell lines using recombinant technique

cell lines are also used as a diagnostic test for the virus, such as human cytomegalovirus, and to determine antiviral agents by testing the capability of a modified gene to infect the cells. The cell lines have which can be impaired in cell lines immortalised by other being able to support viral replication. The cells remain ally suitable for viral/vaccine cultivation

10 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

99.3%; Score 4015.4; DB 6; Length 4070;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGCGCTGCGTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGACCCCGCGATG 65
AGCGCTGCGTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGACCCCGCGATG 78
CGCGTCCCGCTGCGGAGCCGCTGCGTCCCTGCTGCGCAGCCACTACCGGAGTG 125
CGCGTCCCGCTGCGGAGCCGCTGCGTCCCTGCTGCGCAGCCACTACCGGAGTG 138
CGCTGCGCAGCTTCTGCGGCGCTGGGGCCCCAGGGCTGGGCTGGTGCAGCGC 185
CGCTGCGCAGCTTCTGCGGCGCTGGGGCCCCAGGGCTGGGCTGGTGCAGCGC 198
GACCCCGCGCTTTCGCGCGCTGCTGGGCCCCAGTGCCCTGGTGGCTGCCCTGGAC 245
GACCCCGCGCTTTCGCGCGCTGCTGGGCCCCAGTGCCCTGGTGGCTGCCCTGGAC 258
CGCGCGCCCCCGCGCCCCCTTCCGCGCTGGTGGCCCCAGTGCCCTGGTGGCTGGT 318
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CTGTGACGGGGCGCGCGGGGGCCCCCGAGGCCCTTACACAGCGTGGCGAGC 438
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CTGCCCAACAGGTGACCGACGCTGCGGGGGAGCGGGGGCTGGGGCTGTGCTG 498
CGCGTGGGCGACGACGCTGTGTTTACCTGTGGCAGCGTGGCGCTCTTTGCTG 545
CGCGTGGGCGACGACGCTGTGTTTACCTGTGGCAGCGTGGCGCTCTTTGCTG 558
GCTCCAGCTGCGCTACCGAGTGTGCGGGCGCGCGCTGTACAGCTCGGCTGCC 605
GCTCCAGCTGCGCTACCGAGTGTGCGGGCGCGCGCTGTACAGCTCGGCTGCC 618
CAGGCCCGGGCCCCCGCCACACGCTAGTGGAACCCCGAAGCGCTGGGATCGAACGG 665
CAGGCCCGGGCCCCCGCCACACGCTAGTGGAACCCCGAAGCGCTGGGATCGAACGG 678
TGGAACCATAGCTCAGGGAGCGCGGGGTCCCCCTGGGGCTGCCAGCCCCGGGTGG 725
TGGAACCATAGCTCAGGGAGCGCGGGGTCCCCCTGGGGCTGCCAGCCCCGGGTGG 738
AGGCGCGGGGGCAGTGCCAGCGCAAGTCTGCCGTGGCCAGAGGCCCGAGGCTGGC 785
AGGCGCGGGGGCAGTGCCAGCGCAAGTCTGCCGTGGCCAGAGGCCCGAGGCTGGC 798
GCCCTGAGCCGGAGCGCGCGCTTGGGAGGGGTCTGGGGCCCCACCCGGGAGG 845
GCCCTGAGCCGGAGCGCGCGCTTGGGAGGGGTCTGGGGCCCCACCCGGGAGG 858
CGTGGACCGAGTGACCGTGGTCTGTGTGGTGTACCTGCCAGACCCCGCGAGAA 905
CGTGGACCGAGTGACCGTGGTCTGTGTGGTGTACCTGCCAGACCCCGCGAGAA 918

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UB-09-424-686f-1.rng

2AGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 2045
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 2AGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 2058
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 3CACAGCCTGTTTCTGGATTTCAGGTGAACAGCCCTCCAGACCGGTGTGCACCAACATC 3078
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 2AGATCCTCCTGCTGCAGGGCGTACAGGTTTTCACGCATGTGTGCTGCAGTCCCATTT 3125

Db	3079	 TACAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCAATGTGTCTGCAGCT
QY	3126	 CATCAGCAAGTTTGGAGAAACCCACATTTTCTCTGCGCGTCACTCTCTGACACG
Db	3139	 CATCAGCAAGTTTGGAGAAACCCACATTTTCTCTGCGCGTCACTCTCTGACACG
QY	3186	 CTCTGTACTCCATCCTGAAAGCCCAAGAACGCAGCGGATGTCGCTGGGGGCCCAAG
Db	3199	 CTCTGTACTCCATCCTGAAAGCCCAAGAACGCAGCGGATGTCGCTGGGGGCCCAAG
QY	3246	 GCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGT
Db	3259	 GCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGT
QY	3306	 CTGACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCC
Db	3319	 CTGACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCC
QY	3366	 CAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGCGACGC
Db	3379	 CAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGCGACGC
QY	3426	 GCACTGCCCTCAGACTTCAAGACCATCCTGGAATGATGGCCACCCGCCCAACAGC
Db	3439	 GCACTGCCCTCAGACTTCAAGACCATCCTGGAATGATGGCCACCCGCCCAACAGC
QY	3486	 GAGAGCAGACACAGCAGCCCTGTACGCCGGCTCTACGTCCACAGGAGGGAG
Db	3499	 GAGAGCAGACACAGCAGCCCTGTACGCCGGCTCTACGTCCACAGGAGGGAG
QY	3546	 CCCACACCCAGGCCGCACCGCTGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCC
Db	3559	 CCCACACCCAGGCCGCACCGCTGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCC
QY	3606	 TGCACTGCCGCTGAAGGCTGAGTGTCCGCTGAGGCCCTGAGCGAGTGTCTCCAGC
Db	3619	 TGCACTGCCGCTGAAGGCTGAGTGTCCGCTGAGGCCCTGAGCGAGTGTCTCCAGC
QY	3666	 CTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCT
Db	3679	 CTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCT
QY	3726	 CAGGGCCAGTTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATA
Db	3739	 CAGGGCCAGTTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATA
QY	3786	 CCCCAGATTGCGCCATTGTTACCCCTGCGCCCTGCCCTCCTTTGCCCTCCACCCCC
Db	3799	 CCCCAGATTGCGCCATTGTTACCCCTGCGCCCTGCCCTCCTTTGCCCTCCACCCCC
QY	3846	 CCAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGAACCA
Db	3859	 CCAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGAACCA
QY	3906	 TGCCCTGTACACAGGCGAGGACCTCTGCACCTGGATGGGGGTCCCTGTGGGTCAAF
Db	3919	 TGCCCTGTACACAGGCGAGGACCTCTGCACCTGGATGGGGGTCCCTGTGGGTCAAF
QY	3966	 GGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAA
Db	3979	 GGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAA

RESULT 5	
AAZ00724	
ID	AAZ00724 standard; DNA; 4015 BP.
XX	
AC	AAZ00724;
XX	
DT	06-OCT-1999 (first entry)
XX	
DE	Human telomerase catalytic domain

catalytic domain; human; quantitation; tumour cell; melanoma; metastases; T-cell lymphoblastoma; chronic myeloid leukemia; acute leukemia; melanoma; pulmonary carcinoma; colon cancer; pr; ss.

3.

11.

98DE-01004372.

98DE-01004372.

[M W.

1408/37.

tumor cells by amplifying mRNA encoding the catalytic subunit e.

1A-B; 26pp; German.

on describes a novel method for the quantitation of tumour ody fluid which comprises (1) enrichment or isolation of in the sample, (2) amplification of mRNA from these cells the catalytic subunit of telomerase and (3) quantifying the plified mRNA. The method is applied to tumour cells derived metastases, e.g. associated with a wide range of tumours such mphoblastoma, chronic myeloid or acute lymphatic leukemia, lmonary carcinoma, cancer of colon or breast etc. This odes a human telomerase protein catalytic domain

5 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 2; Length 4015;

larity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GCGTGGCTCTGTGGCAGCGTGGGAAGCCCTGGCCCCCGGCCACCCCGGATGCC 67
GCGTGGCTCTGTGGCAGCGTGGGAAGCCCTGGCCCCCGGCCACCCCGGATGCC 60

CGTCCCCCGTGGCAGCGTGGCTCCCTGTGGCAGCGACTACCGGAGGTGCT 127
CGTCCCCCGTGGCAGCGTGGCTCCCTGTGGCAGCGACTACCGGAGGTGCT 120

GCTGGCCACGTTGCTGGCGGCTGGGGCCCCAGGGCTGGGGCTGGTGCAGCGCG 187
GCTGGCCACGTTGCTGGCGGCTGGGGCCCCAGGGCTGGGGCTGGTGCAGCGCG 180

CCCGCGGCTTTCCGCGGCTGGTGGCCCCAGTGCCTGGTGGCTGGGACGC 247
CCCGCGGCTTTCCGCGGCTGGTGGCCCCAGTGCCTGGTGGCTGGGACGC 240

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721 GAGGCGGGGGCAGTCCAGCCGAGTCTGCCGTTGCCAAGAGGCCCCAGGCG
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961 GCACACGCGGGCCCCCATCCACATCGCGGCCACCACTGCCCTGGGACACGCC
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1021 CCGGTGTACGCGGAGACCAAGCACTTCTACTCTCCTCAGGCGACAAGGAGCA
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1148 GACCATCTTTCTGGGTTCCAGGCTTGGATGCCAGGACTCCCCCGAGGTTGCC
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1201 GCGCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTGGGAACCA
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1261 GTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA
1328 AGCGGTGTCTGTGCCCGGAGAACGCCCGAGGCTCTGTGGCGGCCCGGAGGAG
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1448 CGGCTTGTGGGCTTGCCTGCGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG
1441 CGGCTTGTGGGCTTGCCTGCGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG
1508 CAACGAACGCGCTTCTCAGGAACAACAAGAGTTCATCTCCCTGGGGAAGCAT
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[illegible]

standard; cDNA; 4015 BP.

(first entry)

Reverse transcriptase (hTRT) cDNA.

reverse transcriptase; human; hTRT; cell proliferation;

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Location/Qualifiers
56. .3454
/*tag= a
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99WO-US007097.

98US-00052864.
98US-00128354.

IN CORP.

0842/52.
2090.

c polypeptide and polynucleotide, useful for increasing tivity in a cell.

Fig 2; 24pp; English.

nucleotide sequence of cDNA encoding human telomerase reverse transcriptase (hTERT, see AAY32090). Human telomerase is a target for and treating diseases relating to cell proliferation and such as cancer, or for increasing the proliferative capacity of a cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an amino acid sequence in which residues 192-323, 200-323, 192-271, 200-271, 222-271, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A method for reducing telomerase activity in a cell involves introducing into the cell a recombinant polynucleotide encoding an hTERT variant having an amino acid sequence in which residues 192-450, 560-565, 637-660, 638-660, 748-764 or 749-764 are deleted. The hTERT polynucleotides are obtained by mutagenesis of the hTERT cDNA.

CC	coding sequence	
XX		
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
	Query Match 99.3%; Score 4015; DB 2; Length 4015;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 4015; Conservative 0; Mismatches 0; Indels 0;	
QY	8 GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCCACACCCCGCG	
DB	1 GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCCACACCCCGCG	
QY	68 GCGCGCTCCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGGGA	
DB	61 GCGCGCTCCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGGGA	
QY	128 GCCGCTGGCCACGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCA	
DB	121 GCCGCTGGCCACGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGTGGTGCA	
QY	188 GGACCCGGCGGCTTCCGCGCGTGGTGCCCGAGTGCCCTGGTGCGGTGCGTGCCCTG	
DB	181 GGACCCGGCGGCTTCCGCGCGTGGTGCCCGAGTGCCCTGGTGCGGTGCGTGCCCTG	
QY	248 ACGGCCGCCGCCCGCGCCCCCTCCTCCGCGCAGGTGTCCTGCCTGAAGGAGCT	
DB	241 ACGGCCGCCGCCCGCGCCCCCTCCTCCGCGCAGGTGTCCTGCCTGAAGGAGCT	
QY	308 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCCTTCGG	
DB	301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCCTTCGG	
QY	368 GCTGCTGGACGGGGCCCGCGGGGCCCCCCCGAGGCCCTTCAACACAGCGTGCG	
DB	361 GCTGCTGGACGGGGCCCGCGGGGCCCCCCCGAGGCCCTTCAACACAGCGTGCG	
QY	428 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGCT	
DB	421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGCT	
QY	488 CCGCGTGGGCGACGACGTGTGTTCACTGCTGGCACGCTGCGCGCTCTTTGT	
DB	481 CCGCGTGGGCGACGACGTGTGTTCACTGCTGGCACGCTGCGCGCTCTTTGT	
QY	548 GGCTCCCACTGCGCCTACCAAGTGTGCGGGCCCGCGCTGTACCAGCTCGGCGC	
DB	541 GGCTCCCACTGCGCCTACCAAGTGTGCGGGCCCGCGCTGTACCAGCTCGGCGC	
QY	608 TCAGGCCCGGCCCGCCACACGCTAGTGGAACCCCGAAGGCGTCTGGATGCGA	
DB	601 TCAGGCCCGGCCCGCCACACGCTAGTGGAACCCCGAAGGCGTCTGGATGCGA	
QY	668 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCCGGG	
DB	661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCCGGG	
QY	728 GAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCCAGGCGT	
DB	721 GAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCCAGGCGT	
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DB	781 TGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTTGSGGCCACCCCGGG	
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DB	841 GCGTGGACCGAGTGACCGTGGTTCTGTGTGTGTCACTGCCAGACCCCGCGA	
QY	908 CACTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCCATCCGTGGG	
DB	901 CACTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCCATCCGTGGG	
QY	968 GCACACGCGGGCCCCCATCACATCGGGGCCACCCAGTCCCTGGGACACGCT	

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|
|AACGTTCCGCAGAGAAAAGAGGGCCGCTGCTCACCTCGAGGGTGAAGCACTGTT 2040
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RESULT 8
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ID AAH45901 standard; DNA; 4015 BP.
XX
AC AAH45901;
XX
DT 06-SEP-2001 (first entry)
XX
DE Human hTERT gene.
XX
KW Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
KW detection; beta-region; diagnosis; cancer; ds.
OS Homo sapiens.
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MANN LA ROCHE & CO AG F.

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'6930/40.

expression of mRNA encoding hTERT, the catalytic subunit of
as an indicator of cancer, by amplifying RNA using primers
y to hTERT gene sequence and quantitating amplified products.

re 5-7; 29pp; English.

sequence is that of the hTERT gene encoding the catalytic
the human telomerase, comprising 16 exons, which is useful in
quantitating hTERT mRNA. The method is useful for detecting
of beta-region (a 182 nucleotide region consisting of exons
the hTERT-mRNA in a human sample for diagnosis and prognosis
the method provides an accurate measure of telomerase activity
ly measuring mRNA that encodes an active hTERT protein

5 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 4; Length 4015;

larity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3841 AGTGGAGACCCCTGAGAAAGGACCCCTGGAGACTCTGGAAATTTGGAGTGACCAAA
QY 3908 CCTGTACACAGGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAT
Db 3901 CCTGTACACAGGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAT
QY 3968 GAGGTGCTGTGGGAGTAAATACTGAATATATAGTATTTTTCAGTTTGAAGAAA
Db 3961 GAGGTGCTGTGGGAGTAAATACTGAATATATAGTATTTTTCAGTTTGAAGAAA
RESULT 10
ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX
AC ABA97534;
XX
DT 05-APR-2002 (first entry)
XX
DE Cancer cell discrimination method related human DNA.
XX
KW Human; telomerase; enzyme; cancer cell discrimination; gene;
KW reverse transcriptase; ds.
XX
OS Homo sapiens.
XX
PN JP2001309791-A.
XX
PD 06-NOV-2001.
XX
PF 02-MAY-2000; 2000JP-00138250.
XX
PR 02-MAY-2000; 2000JP-00138250.
XX
PA (KANE/) KANEUCHI H.
PA (KAMI/) KAMIMORI M.
XX
DR WPI; 2002-134853/18.
XX
PT Discrimination of a cancer cell in a sample tissue, comprises de
PT the expression level of a reverse transcriptase component of te
PT using a hybridization assay.
XX
PS Claim 2; Page 9-10; 16pp; Japanese.
XX
CC The present invention relates to a method for the discrimination
CC cancer cell in a sample tissue, which involves determining the
CC level of a reverse transcriptase component of telomerase in a c
CC constituting the sample tissue by an in situ hybridization of t
CC the enzyme, and judging a cell showing a higher expression leve
CC that of the reverse transcriptase component of telomerase in a
CC cell to be a cancer cell. The present sequence is a human DNA u
CC exemplification of the invention
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 99.3%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0;
QY 8 GCAGCGCTGCGTCCCTGCTGCGGACGCTGGGAGCCCTGGCCCCGGCCACCCCCGCG
Db 1 GCAGCGCTGCGTCCCTGCTGCGGACGCTGGGAGCCCTGGCCCCGGCCACCCCCGCG
QY 68 GCGCGCTCCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGACGCTACCGCGAG
Db 61 GCGCGCTCCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGACGCTACCGCGAG
QY 128 GCCGCTGGCCACGTTCTGTCGGCGCTGGGGCCCCAGGGTGGCGGCTGGTGCA
Db 121 GCCGCTGGCCACGTTCTGTCGGCGCTGGGGCCCCAGGGTGGCGGCTGGTGCA
QY 188 GGACCCGCGCGCTTTCCGCGCGCTGCTGGGCCAGTGCTGCTGCTGCTGCCCTG

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 |||||
 TGGCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCAACAGCCAGGCCGA 3488
 |||||

QY	3488	GAGCAGACACCAGCAGCCCTGTCA	CAGCGGGCTCTACGTC	CCAGGGAGGGAGG
Db	3481	GAGCAGACACCAGCAGCCCTGTCA	CAGCGGGCTCTACGTC	CCAGGGAGGGAGG
QY	3548	CACACCCAGGCCCGCACCGCTGGAGTCT	GAGGCCTGAGTGAGTGTTGGCCGA	
Db	3541	CACACCCAGGCCCGCACCGCTGGAGTCT	GAGGCCTGAGTGAGTGTTGGCCGA	
QY	3608	CATGTCCGGCTGAAGGCTGAGTGTCCGGCT	GAGGCCTGAGCGAGTGTC	CCAGCCA
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCT	GAGGCCTGAGCGAGTGTC	CCAGCCA
QY	3668	GAGTGTCCAGCACACTGCGCTCTTCACTT	CCCCACAGSGTGGCGCTCGGCTCC	
Db	3661	GAGTGTCCAGCACACTGCGCTCTTCACTT	CCCCACAGSGTGGCGCTCGGCTCC	
QY	3728	GGCCAGCTTTTCTCA	CAGGAGCCCGGCTTCCACT	CCCCACATAGGAATAGT
Db	3721	GGCCAGCTTTTCTCA	CAGGAGCCCGGCTTCCACT	CCCCACATAGGAATAGT
QY	3788	CCAGATTGCCCATTGTTCA	CCCCCTCGCCCTCGCCCTTCCAC	CCCCCA
Db	3781	CCAGATTGCCCATTGTTCA	CCCCCTCGCCCTCGCCCTTCCAC	CCCCCA
QY	3848	AGGTGGAGACCTTGAGAAGGACCTTGGAGCT	CTGGGAATTTGGAGTGACCAA	
Db	3841	AGGTGGAGACCTTGAGAAGGACCTTGGAGCT	CTGGGAATTTGGAGTGACCAA	
QY	3908	CCCTGTACACAGGCGAGGACCCCTGCACCT	TGGATGGGGTCCCTGTGGGTCAAAT	
Db	3901	CCCTGTACACAGGCGAGGACCCCTGCACCT	TGGATGGGGTCCCTGTGGGTCAAAT	
QY	3968	GAGGTGCTGTGGGAGTAATACTGAATATATGAT	TTTTTTCAGTTTTTGAAAAA	
Db	3961	GAGGTGCTGTGGGAGTAATACTGAATATATGAT	TTTTTTCAGTTTTTGAAAAA	

RESULT 11

ACC58039
ID ACC58039 standard; cDNA; 4015 BP.

AC ACC58039:

DT 11-AUG-2003 (first entry)

Human telomerase reverse transcriptase cDNA.

KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contr;
 KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
 KW antiinflammatory; human; gene therapy; gene; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
ET	CDS	56. .3454

PN WO2003035667-A2.

01-MAY-2003.

16-OCT-2002: 2002WO-US033065.

AA 22-OCT-2001: 2001US-0345326P.

FR 22-UCI-2001; 2001US-0343326P;
PR 20-FEB-2002; 2002US-0359196P.

FK Z0-FEB-2002; 2002US-0333196P.
PR 22-MAY-2002; 2002US-0383195P.

PA (UYRP) UNIV ROCHESTER.

XX
PI Rowley PT:XX
TJ

03336/38.
42384.

e-stranded short interfering RNA having sense and antisense ds which are complementary to each other and to target nucleic telomerase RNA or mRNA encoding telomerase reverse se.

Fig 3A-B; 37pp; English.

sequence is that of human telomerase reverse transcriptase . The invention relates to the discovery that double-stranded RNAs, such as short interfering RNAs (siRNA), which target RNA or TERT mRNA are capable of inhibiting telomerase nhibition of telomerase in cancer cells leads to telomere end-to-end chromosomal fusion, and apoptosis. Interference of activity can also be used for treatment of infertility, for on or sterilisation, for immunosuppression, for treatment of site and fungal infections, and in antiinflammatory therapies. se is active in a limited number of cell types, e.g. tumour line cells, certain stem cells of the haematopoietic system, T , sun-damaged skin, and proliferative cervix, most normal ot affected by telomerase RNA interference therapy

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 7; Length 4015;

ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GCGTCCCCGCTGCCGAGCCGCTGCGCTCCCTGCTGCGGAGCCACTACCGGAGTGCT 120
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GAGTGTGCAGAGGCTGTGCGAGCGCGCGGCGAAGACGTCGCTGCTGCTGCTGCTGCTG 367
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Db 2821 GCCGGCCCCAGGCCCTATTTCCCTGGTGGGCGCTGCTGCTGATACCCCGACCCCT
QY 2888 GCAGAGCGACTACTCCAGCTATGCCCGGACCTTCCATCAGAGCCAGTCTCACCTT
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTTCCATCAGAGCCAGTCTCACCTT
QY 2948 CCGCTTCAAGGCTGGAGGAAACATGCGTTCGCAAACTCTTTGGGGTCTTGGGGCT
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QY 3008 TCACAGCCTGTTTCTGGATTTGAGGTGAACAGCCTCCAGACGGTGTGACCCAA
Db 3001 TCACAGCCTGTTTCTGGATTTGAGGTGAACAGCCTCCAGACGGTGTGACCCAA
QY 3068 CAAGATCCTCTGCTGTCAGGCGTACAGGTTTACGATGCTGCTGAGCTCCC
Db 3061 CAAGATCCTCTGCTGTCAGGCGTACAGGTTTACGATGCTGCTGAGCTCCC
QY 3128 TCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGGCTCATCTCTGACACGGC
Db 3121 TCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGGCTCATCTCTGACACGGC
QY 3188 CTGCTACTCCATCCTGAAAGCCAAAGAACCGCAGGGATGCTGCTGGGGCCAAAGG
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Db 3301 GACTCGACACCGTGTCACTACGTGCCACTCTCTGGGTCATCTCAGGACAGCCCF
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QY 3428 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTGATGCCACCCCGCCACAGCCF
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Db 3721 GGGCCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATAG
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QY 3848 AGGTGGAGACCTTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAA
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11:43:35 2004

us-09-424-686f-1.rng

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andard; cDNA; 4015 BP.

(first entry)

erase reverse transcriptase cDNA.

reverse transcriptase; TERT: enzyme; RNA interference;
fering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
essive; antiinfertility; fungicide; antiparasitic;
atory; human; gene therapy; gene; ss.

• 62

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Location/Qualifiers
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/product= "TERT"
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5-A2.

; 2002WO-US033146.

; 2001US-0345326P.
; 2002US-0359196P.
; 2002US-0383195P.

V ROCHESTER.

03289/38.
42063.

ic acid encoding or comprising interfering RNAs which target RNA, useful for inhibiting telomerase activity for treating fertility and disorders of the immune system.

Fig 3; 52pp; English.

sequence is that of human telomerase reverse transcriptase. The invention relates to the discovery that double-stranded RNAs, such as short interfering RNAs (siRNA), which target RNA or TERT mRNA are capable of inhibiting telomerase inhibition of telomerase in cancer cells leads to telomere end-to-end chromosomal fusion, and apoptosis. Interference of activity can also be used for treatment of infertility, for on or sterilisation, for immunosuppression, for treatment of site and fungal infections, and in anti-inflammatory therapies. se is active in a limited number of cell types, e.g. tumour line cells, certain stem cells of the haematopoietic system, T sun-damaged skin, and proliferative cervix, most normal ot affected by telomerase RNA interference therapy

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 7; Length 4015;
ilarity 100.0%; Pred.No. 0;
Conservative 0; Mismatches 0; Indels 0

AGCGCTGCGTCCTGCTGCGGCA CGTGGGAAGCCCTGGCCCCCGGCCA CCCCCGGATGCC 67

Db	1	GCAGCGCTGCGTCTCTGCTGGCA	CGTGGGAAGCCCTGGCCCCGGCCACACCCCGG
Qy	68	GCGCGCTCCCGCTGCGAGCCG	TGCGCTCCCTGCTGGCAGCCACTACCGCGA
Db	61	GCGCGCTCCCGCTGCGAGCCG	TGCGCTCCCTGCTGGCAGCCACTACCGCGA
Qy	128	GCCGCTGGCCACGTTGTCGGCG	CCCTGGGGCCCCAGGGCTGGCGGCTGGTGCA
Db	121	GCCGCTGGCCACGTTGTCGGCG	CCCTGGGGCCCCAGGGCTGGTGCA
Qy	188	GGACCCGGCGGCTTTCGGCGCG	CTGGTGAGCCAGTGCCCTGGTGCCCTG
Db	181	GGACCCGGCGGCTTTCGGCGCG	CTGGTGAGCCAGTGCCCTGGTGCCCTG
Qy	248	ACGGCCGCCCCCGCGCCCCCT	CTCTCCGCGCAGGTGTCTCTGCTGAAGGAGCT
Db	241	ACGGCCGCCCCCGCGCCCCCT	CTCTCCGCGCAGGTGTCTCTGCTGAAGGAGCT
Qy	308	CCGAGTGCTGCAGAGGCTGTG	CGAGCGCGCGGCGAAGAACGTGCTGGGCCCTTCGG
Db	301	CCGAGTGCTGCAGAGGCTGTG	AGCGCGCGGCGAAGAACGTGCTGGGCCCTTCGG
Qy	368	GCTGCTGGA	CGGGGCGCGGGGGCCCCCGAGGCCCTTCA
Db	361	GCTGCTGGA	CGGGGCGCGGGGGCCCCCGAGGCCCTTCA
Qy	428	CCTGCCAAACACGGTGACCG	ACGACTGCGGGGAGCGGGGCTGGGGCTGCT
Db	421	CCTGCCAAACACGGTGACCG	ACGACTGCGGGGAGCGGGGCTGGGGGCTGCT
Qy	488	CGCGTGGCGACGAGCTGCT	TGGTTCACTGCTGGCACGCTGCGGCTCTTTGT
Db	481	CGCGTGGCGACGAGCTGCT	TGGTTCACTGCTGGCACGCTGCGGCTCTTTGT
Qy	548	GGCTCCAGCTGCGCTTAC	AGGTGTGCGGCGCGCGCTGTACCAGCTCGGCG
Db	541	GGCTCCAGCTGCGCTTAC	AGGTGTGCGGCGCGCGCTGTACCAGCTCGGCG
Qy	608	TCAGGCCCGCCCCCGCCAC	ACGCTAGTGAGACCCCGAAGGCGCTTGGGATGCGA
Db	601	TCAGGCCCGCCCCCGCCAC	ACGCTAGTGAGACCCCGAAGGCGCTTGGGATGCGA
Qy	668	CTGGAACCATAGCTCAGG	AGGCCCGGGTCCCCCTGGGCCCTGCCAGCCCCCGG
Db	661	CTGGAACCATAGCTCAGG	AGGCCCGGGTCCCCCTGGGCCCTGCCAGCCCCCGG
Qy	728	GAGCGCGGGGCGAGTGCC	AGCCGAAGTCTGCCCTTGCCCCAAGAGGCCAGGCC
Db	721	GAGCGCGGGGCGAGTGCC	AGCCGAAGTCTGCCCTTGCCCCAAGAGGCCAGGCC
Qy	788	TGCCCCTGAGCCGAGCGG	ACGCCCTTGCGCAGGGGTCTGGGCCACCCCGG
Db	781	TGCCCCTGAGCCGAGCGG	ACGCCCTTGCGCAGGGGTCTGGGCCACCCCGG
Qy	848	CGCTGGACCGAGTGACCG	TGGTTTCTGTGTGGTGTCACCTGCCAGACCCCGCGA
Db	841	CGCTGGACCGAGTGACCG	TGGTTTCTGTGTGGTGTCACCTGCCAGACCCCGCGA
Qy	908	CACCTCTTTGGAGGTGCG	CTCTTGGCA
Db	901	CACCTCTTTGGAGGTGCG	CTCTTGGCA
Qy	968	GCACACCGGGGCCCCCAT	CCACATCGCGGCCACCACTCCCTGGGACACGCC
Db	961	GCACACCGGGGCCCCCAT	CCACATCGCGGCCACCACTCCCTGGGACACGCC
Qy	1028	CCCGGTGTACGCGGAGAC	CAAGCACTTCTCTACTCTCTCAGGCGACAAGGAGCA
Db	1021	CCCGGTGTACGCGGAGAC	CAAGCACTTCTCTACTCTCTCAGGCGACAAGGAGCA
Qy	1088	GCCTCTTCTCTACTCAG	CTCTTGGGCCCCAGCCCTGACTGGCGCTCGGAGGCT

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RESULT 14
ACC4482
ID ACC4482 standard; DNA; 4015 BP.
XX
AC ACC4482;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase gene.
XX
DE Gene; ds; human; telomerase reverse transcriptase; adipogenic c
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine
KW anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 56..3454
FT /*tag= a
FT /product= "telomerase reverse transcriptase"

WO2003031640-A2.
17-APR-2003.
07-OCT-2002; 2002WO-US031635.
06-OCT-2001; 2001US-0327650P.
06-OCT-2001; 2001US-0327651P.
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PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchkonian T;
XX
DR WPI; 2003-421278/39.
DR P-PSDB; ABR58045.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assay;
PT clinical applications, and in the administration of therapeutic
PT particularly for obesity.
XX
PS Disclosure; Page 11-13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte
CC strains that express telomerase reverse transcriptase (TERT- t
CC catalytic subunit of telomerase), and maintain and/or enhance r

und maintain adipogenic capacity of the cell. This sequence the gene encoding the TERT protein. The cell strain can be search to study all aspect of adipogenesis, especially in , researching treatments for e.g. obesity. The cell can also be ntify adipogenesis modulators for use as therapeutic agents mones, growth factors, cytokines, enzymes, cholesterol binding holesterol removing proteins or their combinations. ily, the therapeutic agent may be an adipocytokine, preferably l, or insulin

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 7; Length 4015;

ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX
DT 17-JAN-2000 (first entry)

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ON CORP.
V TECHNOLOGY CORP.

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10834/52.
28881.

olynucleotides for human telomerase reverse transcriptase used
ing or treating cancer.

g 1; 31pp; English.

sequence encodes for human telomerase reverse transcriptase
s is the catalytic protein component of telomerase and is also
as hEST2. This correlates with cell proliferative capacity,
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as therapeutic agents, for inhibition of telomerase
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15 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
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; PRIOR APPLICATION DATA:
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; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
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i3
Application US/09402181B
839
MATION:
T: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
OF SEQUENCES: 633
NDENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
Y: San Francisco
ATE: California
NTRY: USA
P: 94111-3834
READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
TWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/09/402,181B
ING DATE: 29-Sep-1997
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: US 08/724,643
ING DATE: 01-OCT-1996
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
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ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/911,312
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/912,951
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/915,503
ING DATE: 14-AUG-1997
PLICATION NUMBER: WO PCT/US97/17885
ING DATE: 01-OCT-1997
Y/AGENT INFORMATION:
E: Ausenhus, Scott L.
ISTRATION NUMBER: 42,271
ERENCE/DOCKET NUMBER: 015389-002620US
UNICATION INFORMATION:
EPHONE: (415) 576-0200
EFAX: (415) 576-0300
FOR SEQ ID NO: 343:
3 CHARACTERISTICS:

LENGTH: 4037 base pairs
TYPE: nucleic acid
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Matches 4028; Conservative 4; Mismatches 3; Indels 0;
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Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT c
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US-09-721-456-343

Query Match 99.7%; Score 4028.6; DB 4; Length 4037;
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; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor

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Lingner, Joachim
Yakamura, Toru
Chapman, Karen B.
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QUENCES: 727

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300 Embarcadero Center, Eighth Floor
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Db	1	GCAGCGCTGCGTCTCTGTGGGCACGTGGGAAGCCCTGCGCCCCGGGCCACCCCCGCG
Qy	68	GGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG
Db	61	GGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG
Qy	128	GCCGCTGGCCACGTTCTGTGCGCGCCCTGGGGCCCCAGGGCTGGCGCTGGTGAG
Db	121	GCCGCTGGCCACGTTCTGTGCGCGCCCTGGGGCCCCAGGGCTGGCGCTGGTGAG
Qy	188	GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCACTGCCCTGGTGTGCGTGCCCTGG
Db	181	GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCACTGCCCTGGTGTGCGTGCCCTGG
Qy	248	ACGGCCGCCCCCGCGCCCCCTCTTCCGCGCAGGTGTCTCGCTGAAGGAGCTG
Db	241	ACGGCCGCCCCCGCGCCCCCTCTTCCGCGCAGGTGTCTCGCTGAAGGAGCTG
Qy	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGCGCAAGAACGTGTGGCCTTCGGCT
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGGCGCGCAAGAACGTGTGGCCTTCGGCT
Qy	368	GCTGTGACGGGGCCCGGGGGCCCCCGAGGCCTTCACCACCACGCTGCGC
Db	361	GCTGTGACGGGGCCCGGGGGCCCCCGAGGCCTTCACCACCACGCTGCGC
Qy	428	CCTGCCCAACACGCTGACCGACGCACTGGGGGGAGCGGGGCGTGGGGGCTGCTG

'GCCAACACGGTGACCGACGCAC'TGCGGGGAGCGGGCGTGGGGGCTGCTGCTGG 480
'CGTGGGCGACGACGTGCTGTTTACCTGTGGCACGCTGCGCGCTCTTTGTGCTGGT 547
'CGTGGGCGACGACGTGCTGTTTACCTGTGGCACGCTGCGCGCTCTTTGTGCTGGT 540
'TCCCAGCTGCGCCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCGCTGCCAC 607
'TCCCAGCTGCGCCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCGCTGCCAC 600
'GGCG 667
'GGCG 660
'GAACCAATAGCTCAGGAGCGCGGGTCCCGCTGGGCTGCCAGCGCGCGCGCGCGCG 727
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'GCGCGGGGCGAGTCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCAGCGGTGGCGC 780
'CCCTGAGCGGAGCGGACGCGCGTGGGAGGGGTCTGGGCGCGCGCGCGCGCGCG 847
'CCCTGAGCGGAGCGGACGCGCGTGGGAGGGGTCTGGGCGCGCGCGCGCGCGCG 840
'TGGACCGAGTGACCGTGGTCTCTGTGGTGTGACCTGCCAGACCGCGCGCGCGCG 907
'TGGACCGAGTGACCGTGGTCTCTGTGGTGTGACCTGCCAGACCGCGCGCGCGCG 900
'CTCTTTGGAGGGTGCGCTCTCTGGCACCGCGCGCGCGCGCGCGCGCGCGCGCG 967
'CTCTTTGGAGGGTGCGCTCTCTGGCACCGCGCGCGCGCGCGCGCGCGCGCGCG 960
'CCAGCG 1027
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'GGTGACCGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACCAAGGAGCAGCTGG 1087
'GGTGACCGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACCAAGGAGCAGCTGG 1080
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'CATCTTCTGGGTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
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'CCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC 1327
'CCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC 1320
'CGGTGTCTGTCGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGA 1387
'CGGTGTCTGTCGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGA 1380
'AGACCGGT 1447
'AGACCGGT 1440
'CTTCGTGCGGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1507
'CTTCGTGCGGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1500
'CGAAGCGCGCGCTTCTCAGGAACACCAAGAGTTTCTCTCCCTGGGGAAGCATGCCAA 1567
'CGAAGCGCGCGCTTCTCAGGAACACCAAGAGTTTCTCTCCCTGGGGAAGCATGCCAA 1560

1568 GCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGGGACTGCGCTTGGCT
1561 GCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGGGACTGCGCTTGGCT
1628 GAGCCCGAGGGGTTGGCTGTGTTCCGGCCGAGAGCA CCGTCTCGTGGAGAGAT
1621 GAGCCCGAGGGGTTGGCTGTGTTCCGGCCGAGAGCA CCGTCTCGTGGAGAGAT
1688 CAAGTTCTGCACTGGCTGATGAGTGTGTACGTCTCGAGTGTCTCAGGTCTTTT
1681 CAAGTTCTGCACTGGCTGATGAGTGTGTACGTCTCGAGTGTCTCAGGTCTTTT
1748 TGTACCGGAGACCA CCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGT
1741 TGTACCGGAGACCA CCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGT
1808 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGAG
1801 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGAG
1868 GGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCGCTGCTGACGTCCAG
1861 GGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCGCTGCTGACGTCCAG
1928 CTTTATCCCCAAGCTGACGGGCTGCGGCGGATTTGTGAACATGAGCTACGTCTG
1921 CTTTATCCCCAAGCTGACGGGCTGCGGCGGATTTGTGAACATGAGCTACGTCTG
1988 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGGC
1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGGC
2048 CAGCGTGTCTCAACTA CAGAGGGGCGCGGCGCGCGCGCGCGCGCGCTCTGCTG
2041 CAGCGTGTCTCAACTA CAGAGGGGCGCGGCGCGCGCGCGCGCGCGCTCTGCTG
2108 CTTGGAAGGATA TCCACAGGCGCTGGGCGCACTTCTGCTGCTGCTGCGGGCGCG
2101 CTTGGAAGGATA TCCACAGGCGCTGGGCGCACTTCTGCTGCTGCTGCGGGCGCG
2168 GCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGCGGCGCGTACGACACCAT
2161 GCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGCGGCGCGTACGACACCAT
2228 GGACAGGCTCAGCGAGGTCTATCGCCAGCATCATCAAAACCCAGAAACAGTACTG
2221 GGACAGGCTCAGCGAGGTCTATCGCCAGCATCATCAAAACCCAGAAACAGTACTG
2288 TCGGTATGCCGTGGTCCAGAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCA
2281 TCGGTATGCCGTGGTCCAGAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCA
2348 CGTCTCTACCTTGACAGACCTTCCAGCGGTACATGCGACAGTTCTGCTGCTCACCTG
2341 CGTCTCTACCTTGACAGACCTTCCAGCGGTACATGCGACAGTTCTGCTGCTCACCTG
2408 GACCAGCGCGCTGAGGAGTCCGTCTCATCGAGCAGAGCTCTCTCCCTGAATGAG
2401 GACCAGCGCGCTGAGGAGTCCGTCTCATCGAGCAGAGCTCTCTCCCTGAATGAG
2468 CAGTGGCGCTCTTCGACGTCTTCTACGCTTCCAGCGGTACATGCGCGCGCGCGCAT
2461 CAGTGGCGCTCTTCGACGTCTTCTACGCTTCCAGCGGTACATGCGCGCGCGCGCAT
2528 CAAGTCTCTACGTCCAGTCCAGGGGATCCCGCAGGGGCTCCATCTCTCCACGCTG
2521 CAAGTCTCTACGTCCAGTCCAGGGGATCCCGCAGGGGCTCCATCTCTCCACGCTG
2588 CAGCGTGTGCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGAC
2581 CAGCGTGTGCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGAC

us-09-424-686f-1.rni

Db	3721	GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
Qy	3788	CCAGATTGCGCATTTGTTCACCCCCTCGCCCTGCCCCCTCCTTTGCCTTCCACCCCCA
Db	3781	CCAGATTGCGCATTTGTTCACCCCCTCGCCCTGCCCCCTCCTTTGCCTTCCACCCCCA
Qy	3848	AGGTGGAGACCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAA
Db	3841	AGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAA
Qy	3908	CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAT
Db	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAT
Qy	3968	GAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA
Db	3961	GAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA

RESULT 6
US-08-854-050-224
; Sequence 224, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

OR SEQ ID NO: 224:

CHARACTERISTICS:

4015 base pairs

5' to 3'

3SS: single

linear

PE: CDNA

CDS

56..3454

ORF1: /product= "hTRT"

ORF2: /note= "human telomerase reverse

ORF3: transcriptase (hTRT) catalytic protein

ORF4: component"

1

Similarity: 99.3%; Score 4015; DB 3; Length 4015;

Identity: 100.0%; Pred. No. 0;

Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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AGTGGCCACAGTTGCTGGCGCGCTGGGGCCCGCAGGGCTGGCGGTGGTGGCAGCGCG 187

|||||

AGTGGCCACAGTTGCTGGCGCGCTGGGGCCCGCAGGGCTGGCGGTGGTGGCAGCGCG 180

|||||

ACCGGGCGGCTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGGCAGCGC 247

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ACCGGGCGGCTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGGCAGCGC 787

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Db 781 TGCCCTTGAGCGGAGCGGACGCCCGTTGGGAGGGGTCTCTGGGCCACCCCGG

QY 848 GCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCCGCGA

Db 841 GCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCCGCGA

QY 908 CACCTCTTTGGAGGGTGCGCTCTCTGGCAGCGGCCACTCCCACCCATCCGTGGG

Db 901 CACCTCTTTGGAGGGTGCGCTCTCTGGCAGCGGCCACTCCCACCCATCCGTGGG

QY 968 GCACACGCGGGCCCCCATCCACATCGGCGCCACCACTCCCTGGGACACGCC

Db 961 GCACACGCGGGCCCCCATCCACATCGGCGCCACCACTCCCTGGGACACGCC

QY 1028 CCCGGTGTACGCGGAGACCAAGCACCTTCTCTACTCTCTCAGGCGACCAAGAGCA

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QY 1088 GCCCTCTCTCTACTACTAGCTCTCTAGGCGCCAGCTGACTGGCGCTCGAGGCT

Db 1081 GCCCTCTCTCTACTACTAGCTCTCTAGGCGCCAGCTGACTGGCGCTCGAGGCT

QY 1148 GACCATCTTTCTGGGTTCCAGGCCCTTGATGCCAGGGACTCCCCCGCAGGTTGCC

Db 1141 GACCATCTTTCTGGGTTCCAGGCCCTTGATGCCAGGGACTCCCCCGCAGGTTGCC

QY 1208 GCGCCAGCGCTACTGGCAATGGGCGCCCTGTTTCTGGAGCTGCTGGGAACCA

Db 1201 GCGCCAGCGCTACTGGCAATGGGCGCCCTGTTTCTGGAGCTGCTGGGAACCA

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Db 1261 GTGCCCCCTACGCGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTGCT

QY 1328 AGCGGTGTGTGTGCGCGGAGAGCGCCAGGGCTCTGTGGCGGCCCGCGAGGA

Db 1321 AGCGGTGTGTGTGCGCGGAGAGCGCCAGGGCTCTGTGGCGGCCCGCGAGGA

QY 1388 CACAGACCGCGCTGCGCTGGTGCAGCTGCTCCGCGAGCACAGCGCCCTGGCA

Db 1381 CACAGACCGCGCTGCGCTGGTGCAGCTGCTCCGCGAGCACAGCGCCCTGGCA

QY 1448 CGGCTTCTGCGGGCTGCGCTGCGCGGCTGCTGCGCGGCTGCTGGGGCTC

Db 1441 CGGCTTCTGCGGGCTGCGCTGCGCGGCTGCTGCGCGGCTGCTGGGGCTC

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Db 1501 CAACGACCGCGCTTCTCTCAGGAACACCAAGAGTTCTATCTCTCTGGGGAAGCA

QY 1568 GCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTGGCT

Db 1561 GCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTGGCT

QY 1628 GAGCCAGGGGTGGCTGTGTTCCGCGCCGAGAGCACCTCTGCGTGAGGAGAT

Db 1621 GAGCCAGGGGTGGCTGTGTTCCGCGCCGAGAGCACCTCTGCGTGAGGAGAT

QY 1688 CAAGTTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTT

Db 1681 CAAGTTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTT

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Db 1741 TGTACGAGGACCACTGTTTCAAGAAACAGGCTCTTTTCTACCGGAAGAGTGT

QY 1808 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGAGCTGCGGAG

Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGAGCTGCGGAG

QY 1868 GGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAG

11:43:35 2004

us-09-424-686f-1.rni

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QY	3008	TCACAGCCTGTTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAA
Db	3001	TCACAGCCTGTTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAA
QY	3068	CAAGATCCTCCTGCTGCAAGCGGTACAGGTTTCACGCATGTGTCTGCAGCTCCC
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QY	3128	TCAGCAAGTTTGGAAAGAACCCCAACATTTTTCCTGCGCGTCATCTCTGACACGGC
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QY	3188	CTGCTACTCCATCCTGAAAGCCAAAGAACGCAGGGATGTGCTGGGGGCCAAGGG
Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGAACGCAGGGATGTGCTGGGGGCCAAGGG
QY	3248	CGGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGTCACCAAGCATTCCTGCT
Db	3241	CGGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCTGTGTCACCAAGCATTCCTGCT
QY	3308	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAA
Db	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAA
QY	3368	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAA
Db	3361	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAA
QY	3428	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCA
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCA
QY	3488	GAGCAGACACCAAGCAGCCCTGTCAAGCCGGGCTCTACGTCCCAGGAGGGAGGG
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAAGCCGGGCTCTACGTCCCAGGAGGGAGGG
QY	3548	CACACCCAGGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTGTTTGGCCGA
Db	3541	CACACCCAGGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTGTTTGGCCGA
QY	3608	CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCA
Db	3601	CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCA
QY	3668	GAGTGTCAGCACACCTGCCGCTTCACTTCCCACAGGCTGGCGCTCGGCTCC
Db	3661	GAGTGTCAGCACACCTGCCGCTTCACTTCCCACAGGCTGGCGCTCGGCTCC
QY	3728	GGCCAGTTTTTCTCACCAAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
Db	3721	GGCCAGTTTTTCTCACCAAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
QY	3788	CCAGATTCGCAATGTTTCAACCCCTCGCCCTGCCCTTGCCTTCCACCCCCCA
Db	3781	CCAGATTCGCAATGTTTCAACCCCTCGCCCTGCCCTTGCCTTCCACCCCCCA
QY	3848	AGGTGGAGACCCTGAGAAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAAA
Db	3841	AGGTGGAGACCCTGAGAAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAAA
QY	3908	CCCTGTACAGGGCAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAAT
Db	3901	CCCTGTACAGGGCAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAAT
QY	3968	GAGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAAA
Db	3961	GAGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAAA

RESULT 7
US-09-430-323-224
; Sequence 224, Application US/0943030323

INFORMATION:

INVENTION: No. 6309867el Telomerase

INDENCE ADDRESS:

FEET: Two Embarras

1: San Francisco
TE: California

INRI: UNLLED SLA
: 94711

.. READABLE FORM:
ITEM TYPE: FJ CREF:

COMPUTER: IBM PC

**SOFTWARE: PATENT IN
APPROPRIATION DIM?**

PLICATION NUMBER:

CLASSIFICATION: Unclassified

'LICATION NUMBER:

'LICATION NUMBER:

'LICATION NUMBER:

'LICATION NUMBER:

'LICATION NUMBER:

/AGENT INFORMATION

REGISTRATION NUMBER

EVIDENCE/DOCKET NUMBER
UNIFICATION INFORMATION

EFHONB: (413) 576-0000
EFAY: (415) 576-0000

OR SEQ ID NO: 227

GL: 405 page 6

ANDEDNESS: single

TYPE: CDNA

E/KEY: CDS

ER INFORMATION:

nscriptase (hTRT)

DESCRIPTION: SEQ

99.38%

Conservative

GGCTGCGTCCTGCTGG

05165LJ05G5LN555

CONCLUSIONS

[illegible]

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; EARLIER FILING DATE: 1998-03-31
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Patent No. 6440735
GENERAL INFORMATION:
APPLICANT: Gaeta, Federico C.A.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Imm
TITLE OF INVENTION: Response to a Telomerase Antigen
FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: US/09/675,321
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
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LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1

Query Match 99.3%; Score 4015; DB 4; Length 4015;
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Matches 4015; Conservative 0; Mismatches 0; Indels 0;

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; Patent No. 644650
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,919
; FILING DATE: 31-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
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; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
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Accession Number: 42,058
Docket Number: 015389-003600US
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(415) 576-0200
(415) 576-0300
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SS: single
linear
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CDS
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ORF Annotation: /product= "human telomerase reverse
ORF Annotation: transcriptase (hTRT)"

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QY 3008 TCACAGCCTGTTTCTGGATTGCAAGTGAACAGCCCTCCAGACGGTGTGCACCAA
Db 3001 TCACAGCCTGTTTCTGGATTGCAAGTGAACAGCCCTCCAGACGGTGTGCACCAA
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QY 3128 TCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGTCACTCTGACACGGC
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QY 3728 GGGCCAGCTTTTCTCAAGGAGCCCGCTTCCACTCCCAACATAGGAATAGT
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Publication US/09733294A

171

NOTIFICATION:

Att P. Monia

William Gaarde

isan M. Freier

Edward V. Wencewicz

EDWARD V. MALICEWICZ
ATTENTION: ANTICENTSE MOVIE THEATRE OF SEEN
EXPERIENCE

STONY: NOT II
ZC30 HADL
T. TERN

1: ISPH-0527

NOTIFICATION NUMBER: 0570
DATE: 2000-10-27

; DATE: 2000-12-07

TELEPHONE NUMBER: 09/572,423

DATE: 2000-01-11

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US-09-733-294A-3

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Query Match          99.3%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0;
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QY 2948 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGCAAACTCTTTGGGGCTTTCGGGCT
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGCAAACTCTTTGGGGCTTTCGGGCT
QY 3008 TCACAGCCTGTTTCTGGATTTGACAGTGAACAGCCTCCAGACGGTGTGACCAA
Db 3001 TCACAGCCTGTTTCTGGATTTGACAGTGAACAGCCTCCAGACGGTGTGACCAA
QY 3068 CAAGATCCTCTGCTGAGGCGGTACAGGTTTACGCTTTCAGCATGTGTGCTGAGCTCCC

11:43:35 2004

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3CGTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCACATACCCGCGAGGTGCT 120

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QY	1328	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCCGAGGA
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QY	1388	CACAGACCCCCGTTCGCTGGTGCTGCTCCGCCAGCACAGCAGCCCCCTGGCA
Db	1381	CACAGACCCCCGTTCGCTGGTGCTGCTCCGCCAGCACAGCAGCCCCCTGGCA
QY	1448	CGGCTTCGTGCGGGCTGCCTGCGCGGGCTGGTGCCCCCAGGCCCTCTGGGGCTC
Db	1441	CGGCTTCGTGCGGGCTGCCTGCGCGGGCTGGTGCCCCCAGGCCCTCTGGGGCTC
QY	1508	CAACGAAAGCCGCTTCCTCAGGAACACCAAGAAAGTTTCATCTCCCTGGGAAGCA
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QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGCGGACTCGGCTTTGGCT
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Db	1621	GAGCCCCAGGGTTGGCTGTGTTCCGGCCGACAGCACCGTCTCGTGAGGAGAT
QY	1688	CAAGTTCCCTGACTGGCTGATGAGTGTACGTGCTCGAGCTGCTCAGGTCTTT
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QY	1748	TGTCACGGAGACACGTTTCAAAGAAACAGGCTCTTTTCTACCCGGAAGAGTGT
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QY	1868	GGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAG
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QY	2168	GCCGCTGAGCTGTACTTTTGTCAAGGTGGATGTGACGGGCGGCTACGACACCAT
Db	2161	GCCGCTGAGCTGTACTTTTGTCAAGGTGGATGTGACGGGCGGCTACGACACCAT
QY	2228	GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTG
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QY	3428	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGSCCACCCTCCACAGCCA
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGSCCACCCTCCACAGCCA
QY	3488	GAGCAGACACCAGCAGCCCTGTCAAGCCGGGCTCTACGTCCCAGGGAGGGAGG
Db	3481	GAGCAGACACCAGCAGCCCTGTCAAGCCGGGCTCTACGTCCCAGGGAGGGAGG
QY	3548	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGA
Db	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGA
QY	3608	CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCA
Db	3601	CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCA
QY	3668	GAGTGTCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGTCGGCTCC
Db	3661	GAGTGTCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGTCGGCTCC
QY	3728	GGGCCAGCTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
Db	3721	GGGCCAGCTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
QY	3788	CCAGATTGCGCAATGTTCAACCCCTCGCCCTGSCCTCCTTTGCCCTCCACCCCCA
Db	3781	CCAGATTGCGCAATGTTCAACCCCTCGCCCTGSCCTCCTTTGCCCTCCACCCCCA
QY	3848	AGGTGGAGACCTTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAA
Db	3841	AGGTGGAGACCTTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAA
QY	3908	CCCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAAT
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QY	3968	GAGGTGCTGTGGGAGTAAATACTGAATATATAGTTTTTTTCAGTTTTGAAAAAA
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RESULT 15

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; Sequence 1, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NO. 6617110-2000

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QY	548	GGTCTCCAGCTGCGCCTACCAAGGTGTGCGGGCCCGCGCTGTACCAGCTCGCGC
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QY	908	CACCTCTTTGGAGGGTGCGCTCTCTGGCACGGGCCACTCCCCACCCATCCGTGGG
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QY	1388	CACAGACCCCCCGTCCGCTGGTGAGTGTCTCCGCCAGCACAGCAGCCCCCTGGCA

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GenCore version 5.1.6
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US-10-325-810-343

; Sequence 343, Application US/10325810

; Publication No. US20030204069A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 633

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/325,810

; FILING DATE: 20-Dec-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,181

; FILING DATE: 29-Sep-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

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>ING DATE: 06-MAY-1997
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5ISTRATION NUMBER: 42,271
ERENCE/DOCKET NUMBER: 015389-002620US
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LEFAX: (415) 576-0300
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3668 QY GAGTGTCCAGCACACCTGCGGTCTTCACTTCCCAAGGCTGGCGCTCGGCTCCA
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AAAAAAAAAAAA 4042
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Publication US/09733294A

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NOTES:

att P. Monia

William Gaard.

usan M. Freier

Edward V. Wancewicz

ANTISENSE MODULATION OF TERT EXPRESSION

E: ISPH-0527

CATION NUMBER: US/09/733,294A

3 DATE: 2000-12-07

FILE: 4000 12 07
 FILE NUMBER: 09/572,423

DATE: 2000-05-16

ID NOS: 108

no sapiens

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6) ... (3454)

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99.3%; Score 4015; DB 9; Length 4015;
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ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

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[illegible]

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| DB | 361 | GCTGCTGGACGGGGCCCGGGGGGGCCCCCGAGGCGCTTCAACCACCAAGCGTGC | |
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| QY | 488 | CCGCGTGGGCGACGACGCTGCTGGTTCACTGCTGGCACGCTGCGCGCTCTTTGT | |
| DB | 481 | CCGCGTGGGCGACGACGCTGCTGGTTCACTGCTGGCACGCTGCGCGCTCTTTGT | |
| QY | 548 | GGCTCCAGCTGCGCCTACCAGGTGTGCGGCGCGCGCTGTACCAGCTCGGCGC | |
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| QY | 728 | GAGGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTGTCCTCAAGAGGCCACAGCG | |
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| DB | 1081 | GCCCTCCTTCTACTCAGCTCTCTGAGGCCCGCCTGACTGGCGCTCGGAGGCT | |
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| DB | 1141 | GACCATCTTCTGGGTTCAGGCCCTGGATGCCAGGACTCCCCCGCAGGTTGCC | |
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| QY | 1328 | AGCCGGTGTCTGTGCCCCGGGAGAGCCCCCAGGGCTCTGTGGCGGCCCCCGAGGA | |
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 DATE: 1998-08-03
 ION NUMBER: US 09/052,864
 DATE: 1998-03-31
 ID NOS: 21
 ntIn Ver. 2.0

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 TION: human telomerase reverse transcriptase (hTERT) cDNA
 99.3%; Score 4015; DB 9; Length 4015;
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 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
US-09-953-052-1
; Sequence 1, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcript
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/052,919
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
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; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
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; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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RESULT 6
US-10-325-810-1
; Sequence 1, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harlev, Calvin B.

Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
SEQUENCES: 633
SEQUENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
Y: San Francisco
TE: California
NTRY: USA
94111-3834
READABLE FORM:
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PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
WARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
LICATION NUMBER: US/10/325,810
ING DATE: 20-Dec-2002
SSIFICATION: <Unknown>
PLICATION DATA:
LICATION NUMBER: US/09/402,181
ING DATE: 29-Sep-1997
LICATION NUMBER: US 08/724,643
ING DATE: 01-OCT-1996
LICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
LICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
LICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
LICATION NUMBER: US 08/854,050
ING DATE: 09-MAY-1997
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ING DATE: 14-AUG-1997
LICATION NUMBER: US 08/912,951
ING DATE: 14-AUG-1997
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ING DATE: 14-AUG-1997
LICATION NUMBER: WO PCT/US97/17885
ING DATE: 01-OCT-1997
AGENT INFORMATION:
E: Ausenhus, Scott L.
ISTRATION NUMBER: 42,271
ERENCE/DOCKET NUMBER: 015389-002620US
UNICATION INFORMATION:
EPHONE: (415) 576-0200
EFAX: (415) 576-0300
OR SEQ ID NO: 1:
CHARACTERISTICS:
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nscriptase (hTERT) catalytic protein
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Publication US/10388578
US20030224411A1
TION:
on Corporation
anton, Lawrence
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seph, Gold D.
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TION: Genes that are Up- or Down-Regulated During Differentiation of Hu
TION: Embryonic Stem Cells
: 135/001
ATION NUMBER: US/10/388,578
DATE: 2003-03-13
ID NOS: 139
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no sapiens
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US-10-388-578-1
Query Match 99.3%; Score 4015; DB 13; Length 4015;
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Matches 4015; Conservative 0; Mismatches 0; Indels 0;

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11:43:36 2004

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| QY | 2348 | CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCT |
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| QY | 2408 | GACGAGCCCGTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATGA |
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| QY | 2468 | CAGTGGCCTCTTCGACAGTCTTCTTACGCTTCATGTGCCACACGCGGTGGCGAT |
| Db | 2461 | CAGTGGCCTCTTCGACAGTCTTCTTACGCTTCATGTGCCACACGCGGTGGCGAT |
| QY | 2528 | CAAGTCCCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCT |
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| QY | 2588 | CAGCCTGTCTACGCGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGA |
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T: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.

Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
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NAME/KEY: CDS
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0;
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Qy 188 GGACCCCGCGGCTTTCCCGCGCGCTGGTGGCCCGAGTGCCTGGTGTGCGTGGCCCTGC

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| QY | 1328 | AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAA |
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| QY | 1448 | CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCCTCTGGGGCTCC |
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| QY | 1508 | CAACGAACGCCGCTTCCTCAGGAAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCAI |
| Db | 1501 | CAACGAACGCCGCTTCCTCAGGAAACACCAAGAAAGTTTCATCTCCCTGGGGAAGCAI |
| QY | 1568 | GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACCTGCGCTTGGCTC |
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| QY | 1628 | GAGCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCTGAGGAGATCTC |
| Db | 1621 | GAGCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCTGAGGAGATCTC |
| QY | 1688 | CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCCTT |
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| QY | 1748 | TGTCACGAGACCAACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCT |
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| QY | 1808 | CAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAC |
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RESULT 10
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; Sequence 1, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Imm
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
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; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

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Matches 4015; Conservative 0; Mismatches 0; Indels 0;

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APPLICATION DATA:
PLICATION NUMBER: US/10/054,295
LING DATE: 18-Jan-2002
ASSIFICATION: 536
PLICATION DATA:
PLICATION NUMBER: 08/854,050
LING DATE: <Unknown>
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
ISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
MUNICATION INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 224:
E CHARACTERISTICS:
NGTH: 4015 base pairs
PE: nucleic acid
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ATION:

ALLIANCE
Iron Corporation

ennig, Chris

Lark, A. John

chiff, J. Michael

NTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

NTN: Transplantation and a Carbohydrate Determinant Selection System

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11:43:36 2004

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; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DI
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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; NAME/KEY: CDS
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; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

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Query Match 99.3%; Score 4015; DB 15; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015: Conservative 0; Mismatches 0; Indels 0;

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US-10-044-539-1

; Sequence 1, Application US/10044539

; Publication No. US20030100093A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DI

; THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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  FILING DATE: 11-Jan-2002
  CLASSIFICATION: 435
APPLICATION DATA:
  APPLICATION NUMBER: 08/912,951
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
AGENT INFORMATION:
  AGENT: Apple, Randolph T.
  INVENTOR: RANDOLPH T. APPLE
  REFERENCE/DOCKET NUMBER: 015389-002600US
COMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  FACSIMILE: (415) 576-0300
FOR SEQ ID NO: 1:
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GenCore version 5.1.6
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SUMMARIES

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| | 39.2 | 1826 | 29 | AY407349 | AY407349 Homo sapi |
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| | 22.5 | 1835 | 29 | AY407351 | AY407351 Mus muscu |
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| | 7 | 445 | 11.0 | 492 | 12 | BM824748 | BM824748 |
| | 8 | 419 | 10.4 | 851 | 12 | BG917907 | BG917907 |
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| | 11 | 346.2 | 8.6 | 688 | 14 | CF531121 | CF531121 |
| | 12 | 340.4 | 8.4 | 649 | 14 | CF531069 | CF531069 |
| | 13 | 322 | 8.0 | 599 | 10 | BB618671 | BB618671 |
| | 14 | 317.8 | 7.9 | 664 | 13 | BQ258274 | BQ258274 |
| C | 15 | 316.4 | 7.8 | 340 | 9 | AA811084 | AA811084 |
| | 16 | 290.8 | 7.2 | 614 | 10 | BB651920 | BB651920 |
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| | 19 | 252.2 | 6.2 | 715 | 10 | BE396925 | BE396925 |
| | 20 | 249.6 | 6.2 | 409 | 9 | AA311750 | AA311750 |
| | 21 | 248.8 | 6.2 | 679 | 10 | BE396606 | BE396606 |
| | 22 | 243.2 | 6.0 | 649 | 10 | BE514070 | BE514070 |
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| | 24 | 214 | 5.3 | 344 | 14 | CF531258 | CF531258 |
| | 25 | 208.6 | 5.2 | 779 | 10 | BE268183 | BE268183 |
| | 26 | 203.8 | 5.0 | 336 | 13 | BY775178 | BY775178 |
| | 27 | 203.2 | 5.0 | 343 | 13 | BY783093 | BY783093 |
| | 28 | 200.6 | 5.0 | 338 | 13 | BY784804 | BY784804 |
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| | 32 | 180.2 | 4.5 | 880 | 13 | BU377259 | BU377259 |
| | 33 | 167.6 | 4.1 | 775 | 12 | BI388013 | BI388013 |
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| | 36 | 150.4 | 3.7 | 668 | 14 | CA380121 | CA380121 |
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ALIGNMENTS

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| | | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom | | | | | | | | |
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| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariw | | | | | | | | | |
| | Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B | | | | | | | | | |
| | Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J. | | | | | | | | | |
| | Adams,M.D. and Cargill,M. | | | | | | | | | |
| TITLE | Inferring nonneutral evolution from human-chimp-mouse or | | | | | | | | | |
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| JOURNAL | Science | 302 | (5652) | 1960-1963 | (2003) | | | | | |
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| | Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J. | | | | | | | | | |
| | Adams,M.D. and Cargill,M. | | | | | | | | | |
| TITLE | Direct Submission | | | | | | | | | |

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3ACTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTCTTTTATGTACGG 1755
3ACTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTCTTTTATGTACGG 120
3CCACGTTTCAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGCAAGTTGC 1815
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ANNACGAGCGGGCGCGCGCCCGCCCTCCTGGGCGCTCTGTGCTGGGCTGGACG 480

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QY 2176 AGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCAGG
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Db 601 NNN
QY 2296 CCGTGTCCAGAAAGCGCCCATGGCAGCTCCGCAAGCCTTCAAGAGCCACG
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Db 841 NNN
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Db 961 GCTACGGCGCATGGAGAACAAAGCTGTTGCGGGGATTCGGCGGGACGGGCTGC
QY 2656 GTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGCGAAACCT
Db 1021 GTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGCGAAACCT
QY 2716 GGACCCCTGTCGAGGTGTCCTGAGTATGCGTGGTGGTGAACCTTGCGGAAGA
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3198 COURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone EST 05-FEB-2002
3198 mRNA sequence. IMAGE:5529840
3198.1 GI:18502238

sapiens (human)
sapiens
cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
cases 1 to 925)
AGC <http://mgc.nci.nih.gov/>.
onal Institutes of Health, Mammalian Gene Collection (MGC)
lished (1999)
act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
e Procurement: ATCC
A Library Preparation: Life Technologies, Inc.
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Agencourt Bioscience Corporation
e distribution: MGC clone distribution information can be
i through the I.M.A.G.E. Consortium/LLNL at:
://image.llnl.gov
3: LLAM12208 row: p column: 01
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Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

19.9%; Score 806; DB 12; Length 925;
ilarity 99.2%; Pred. No. 1.5e-89;
Conservative 0; Mismatches 5; Indels 2; Gaps 1;

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Db 2 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGC
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QY 2216 CACCATCCCCAGGACAGGCTCAGGAGGTCTATGCCAGCATCATCAAAACCCCA
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QY 2276 GTACTGCGTGGTGGTATGCCGTGTCCAGAGGCGCCCATGGGCACGTCCG
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QY 2336 CTTCAAGAGCCACGTCTTACCTTGACAGACCTCCAGCCCGTACATGCGACAGTT
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Db 182 CTTCAAGAGCCACGTCTTACCTTGACAGACCTCCAGCCCGTACATGCGACAGTT
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Db 242 TCACCTGCAGGACAGACCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTC
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QY 2456 GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCA
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Db 302 GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCA
|||||
QY 2516 GCGCATCAGGGCAAGTCTTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCAT
|||||
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Db 482 GCGGACGGGTGCTCTGCTGCTTTGGTGGATGATTTCTTGTGGTGACACCTCA
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QY 2696 CCACGGGAAACCTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGCTG
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QY 2756 GAACTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGTGG
|||||
Db 602 GAACTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGTGG
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QY 2816 TTTTGTTCAGATGCCGCGCCCAAGGCTATCCCTGCTGGTGGGCTGCTGCTGGA
|||||
Db 662 TTTTGTTCAGATGCCGCGCCCAAGGCTATCCCTGCTGGTGGGCTGCTGCTGGA
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QY 2876 GACCCCTGGAGTGCAGAGCGACTACTCCAGCTATGCCGACCTCCATCAGAGC
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Db 722 GACCCCTGGAGTGCAGAGCGACTACTCCAGCTATGCCGACCTCCATCAGAGC
|||||
QY 2936 CACCTTCAACCGCGGCTTCAA--GGCTGGAGGAACATGCGTCGCAAA 2981
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Db 782 CACCTTCAACCGCGGCTTCAAAGGCTGGGAAGGAACATGCGTCGCAAA 829
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RESULT 5
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DEFINITION
UI-M-F10-byx-f-12-0-UI.r1 NIH BMAP_F10 Mus musculus cDNA
IMAGE:6400523 5', mRNA sequence.
ACCESSION
BU702370
VERSION
BU702370.1 GI:23627105
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
1 (bases 1 to 851)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection
REFERENCE
AUTHORS
TITLE

blished (1999)
act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
ue Procurement: Dr. Jim Lin, University of Iowa
A Library preparation: Dr. M. Bento Soares, University of Iowa
A Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Sequencing by: Dr. M. Bento Soares, University of Iowa
ne Distribution: MGC clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL at:
://image.llnl.gov
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P)
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Location/Qualifiers
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/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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Conservative 75.1%; Pred. No. 4.9e-52;
Mismatches 0; Gaps 1;
Indels 6; Gaps 1;
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AGCTCCTCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGT 2502
AGCATCTCTATGAATGAGAGCAGCAGCAGCCTGTTGACTTCTTCTGCACTTCTGTC 240
CACCACGCCGTGCGCATCAGGGGCAAGTCCCTACGTCCAGTGCAGGGATCCCGCAGG 2562
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QY 2683 CACCTCACCTCACCCACGCGAAACCTTCTCCTCAGGACCTGGTCCGAGGTGTC
Db 421 CGCCTCACTTGGACCAAGCAAAACCTTCTCCTCAGCACCTGGTCCATGGCGTT
QY 2743 ATGGCTGCGTGGTGAACCTTGGGAAGACAGTGGTGAACCTTCCCTGTAGAAGAC
Db 481 ATGGGTGCATGATAAACTTGCAGAAGACAGTGGTGAACCTTCCCTGTGGAGCCTC
QY 2803 TGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACCGCCCTATTCCTTGGTGC
Db 541 TGGGTGGTGCAGCTCCATACAGCTGCCTGCTCACTGCTGCTTCCCTGGTGTG
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QY 2923 TCAGAGCCAGTCTCACCTTCAACCGCGCTTCAAGGCTGGGAGGAACATGCCGT
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QY 3103 CATGTGTGCT 3112
Db 841 CATGTGTGAT 850

RESULT 6
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DEFINITION
xv57e03.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2
mRNA sequence.
ACCESSION
AW270031
VERSION
AW270031.1 GI:6657061
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Pran
I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution informa
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 416.
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Site_2: NotI; Cloned unidirectionally. Primer:

Library constructed by Life Technologies."

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| ilarity 99.6%; | Pred. No. 1.1e-47; | | |
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| ICCGGCTGAAGGCTAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAAGGCTGA | 3669 | | |
| ICCGGTTGAAGGCTAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAAGGCTGA | 349 | | |
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 F0096335 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-99-E07
 mRNA sequence.
 4748
 4748.1 GI:19181161
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 sapiens
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 cases 1 to 492)
 V.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Y.S.

Frontier Korean EST Project 2001
Completed (2002)
Contact: Kim YS
Research Center
at Research Institute of Bioscience & Biotechnology
Jeon-dong Yuseong-gu, Daejeon 305-333, South Korea
+82-42-860-4470
+82-42-860-4409

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Soares laboratory and it was constructed as des
Bonaldo, M.F., Lennon, G. and Soares, M.B. (199
Research 6(9): 791-806. RNA was prepared from h
cells of SNU-16 culture. SNU-16 cell was obtain
Korean Cell Line Bank (KCLB). SNU-16 was establ
ascitic fluids of Korean patients by Park J.G.
(1990). Cancer Res 50: 2773-2780."

```

ORIGIN

| Query Match | 11.0%; | Score 445; | DB 12; | Length 492; |
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| Best Local Similarity | 100.0%; | Pred. No. 3.3e-45; | | |
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| Db 1 | GTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATG | | | |
| Qy 2835 | CACGGCCTATTCCCTGGTGC GGCTGCTGTGGATACCCGGACCCCTGGAGGTG | | | |
| Db 61 | CACGGCCTATTCCCTGGTGC GGCTGCTGTGGATACCCGGACCCCTGGAGGTG | | | |
| Qy 2895 | GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCCG | | | |
| Db 121 | GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCCG | | | |
| Qy 2955 | AAGCTGGGAGGAACATGCGTCGCAACTCTTTGGGGTCTTTGGCGCTGAAGTG | | | |
| Db 181 | AAGCTGGGAGGAACATGCGTCGCAACTCTTTGGGGTCTTTGGCGCTGAAGTG | | | |
| Qy 3015 | CTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTAC | | | |
| Db 241 | CTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTAC | | | |
| Qy 3075 | CTCCTGCTGCAGCGGTACAGTTTCACGCATGTGTGCTGCAGTCCCATTTCAT | | | |
| Db 301 | CTCCTGCTGCAGCGGTACAGTTTCACGCATGTGTGCTGCAGTCCCATTTCAT | | | |
| Qy 3135 | GTTTGGAAAGAACCCCAATTTTCTGGCGGTCACTCTGTGACACGGCCCTCCCTC | | | |
| Db 361 | GTTTGGAAAGAACCCCAATTTTCTGGCGGTCACTCTGTGACACGGCCCTCCCTC | | | |
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| Db 421 | TCCATCCTGAAGGCCAAGAACGCAG 445 | | | |

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 BG917907
 BG917907.1 GI:14298383
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
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 1 (bases 1 to 851)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.

CTCCGAGGCCGTGCACATGGCTGTGCCACCAAGCATTCCT-GCTCAAGCTGACTCGACA 3316
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TTCTTGAAGCCGACATTGGCTCTGCTACCAGGCCCTCCTGGCTCAAGCTGGCTGCTCA 687

[illegible]

| | | |
|----|------|---|
| QY | 1746 | TATGTCACGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGAAGAGT |
| | | |
| Db | 61 | TATGTCACGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGAAGAGT |
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| QY | 1806 | AGCAAGTTGCAAAAGCATTGGAATCAGACAGCACATTGAAGAGGGTGCAAGCTGCGG |
| | | |
| Db | 121 | AGCAAGTTGCAAAAGCATTGGAATCAGACAGCACATTGAAGAGGGTGCAAGCTGCGG |
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| QY | 1866 | TCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCC |
| | | |
| Db | 181 | TCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCC |
| | | |
| QY | 1926 | CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCC |
| | | |
| Db | 241 | CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCC |
| | | |
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RESULT 11
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 LOCUS
 DEFINITION
 CF531121
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 CF531121
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 IMAGE:30355988 5', mRNA sequence.
 CF531121
 CF531121.1 GI:34583085
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute]
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri]
 1 (bases 1 to 688)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection
 Unpublished (1999)
 CONTACT: Robert Strausberg, ph.D.

CONTACT: ROBERT SCIAUSBERG, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University
 cDNA Library Arrayed by: Dr. M. Bento Soares, University
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy
 (BMAP)

Seq primer: PYX-5.
 Location/Qualifiers
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FEATURES
 source

Bonaldo, Lennon and Soares, Genome Research, 6:7
site 2; Not I; the library was constructed according
1996. Denatured RNA was size fractionated on a 1%
gel. First strand cDNA synthesis was primed with
primer containing a Not I site. Double strand cDNA
size selected according to mRNA size fraction, ligation
with EcoR I adaptor, digested with NotI and then
directionally into pXX-Asc vector. The library titer
sequence located between the Not I site and the

primer containing a Not I site. Double strand cDNA size selected according to mRNA size fraction, 1 with EcoR I adaptor, digested with NotI and then directionally into pYX-Asc vector. The library t sequence located between the Not I site and the

is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

8.6%; Score 346.2; DB 14; Length 688;
Similarity 73.9%; Pred. No. 3.9e-33;
Conservative 0; Mismatches 155; Indels 0; Gaps 0;
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GGCGGCTTGTGCAACCCCGGACCCGAGATCTACCGCACTTTGTTGCCCAATGCCT 242
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TGTGCTGCTGCTGGGCTCACAGCTCCACCTGCGGACCTTTCTTCCACAGGTGC 302
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GCGGCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
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1069 649 bp mRNA linear EST 12-SEP-2003
-FY0-cgp-c-19-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
E:30355746 5', mRNA sequence.
1069
1069.1 GI:34583033
musculus (house mouse)
musculus
Iyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
bases 1 to 649)
MGC http://mgc.nci.nih.gov/.
onal Institutes of Health, Mammalian Gene Collection (MGC)
blished (1999)
act: Robert Strausberg, Ph.D.
1: cgapbs-r@mail.nih.gov
ue Procurement: Dr. Jim Lin, University of Iowa
A Library preparation: Dr. M. Bento Soares, University of Iowa
A Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of
Clone Distribution: Distribution information can be for
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anat
(BMAP)

Seq primer: pYX-5.
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Site_2: Not 1; The library was constructed acc
Bonaldo, Lennon and Soares, Genome Research, 6:
1996. Denatured RNA was size fractionated on a
gel. First strand cDNA synthesis was primed wit
primer containing a Not I site. Double strand c
size selected according to mRNA size fraction,
with EcoR I adaptor, digested with NotI and the
directionally into pYX-Asc vector. The library
sequence located between the Not I site and the
is AGCAGACAG. This library was created for the
Iowa Brain Anatomy Project (BMAP): 'Gene Discov
Developing Mouse Nervous System', supported by
Institute of Mental Health (NIMH), Hemin Chin,
program coordinator."

ORIGIN

Query Match 8.4%; Score 340.4; DB 14; Length 649;
Best Local Similarity 77.3%; Pred. No. 2e-32;
Matches 413; Conservative 0; Mismatches 121; Indels 0;
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QY 167 CTGGCGGCTGTTGTCAGCGCGGGGACCCCGCGGCTTCCCGCGCTGCTGGGGCC
Db 146 CAGCGGCTTGTGCAACCCGGGACCCGAGATCTACCGCACTTTGTTGCCCA
QY 227 GGTGTGCGTCCCTTGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 206 AGTGTGATGCACTGGGGCTCACAGCCTCCACCTGCCGACCTTCTTCCACCA
QY 287 CTGCCTGAAGGAGTGTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCG
Db 266 ATCCCTGAAAGAGCTGTTGGCCAGGGTTGTGTCAGAGACTCTGCGAGCGCAACGA
QY 347 CGTGTGCGCTTCCGCTTCCGCTGCTGTCGAGCGGGGCCCGCGGGGCCCGCGCG
Db 326 CGTGTGCGCTTTCGCTTTCGCTGCTTTCGCTGCTTTCGCTGCTTTCGCTGCT
QY 407 CACCACGAGCTGCGCAGCTACCTGCGCCACACCGGTGACCGACGCTGCGGGG
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QY 467 GCGTGGGGGCTGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG
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QY 527 CTGCGCGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Db 506 CTGTGCTCTTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

act: Robert Strausberg, Ph.D.
 l: cgapbs-r@mail.nih.gov
 Library Preparation: J. Baker (Stanford University)
 A Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 Sequencing by: National Institutes of Health Intramural
 encoding Center (NIHSC)
 ne distribution: NCI-CGAP clone distribution information can be
 d through the I.M.A.G.E. Consortium/LLNL at:
 @image.llnl.gov
 :1845958
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 /note="Vector: pCS105; Site 1: NotI; Site 2: Sali; cDNA
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 Sali/NotI sites using the following 5' adaptor:
 5'-TCGACCAACCGTCCG-3'. Size-selected for average insert
 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

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7.9%; Score 317.8; DB 13; Length 664;
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Conservative 0; Mismatches 177; Indels 45; Gaps 1;

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-----TGAACACAGCCCCACCGCACCTCATGGATT 263

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| | | |
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| QY | 1775 | CAGGCTCTTTTCTACCGGAAGAGTGCTCTGGAGCAAGTTGC 1815 |
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| ORGANISM | Homo sapiens | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom | |
| TITLE | 1 (bases 1 to 340) | |
| JOURNAL | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . | |
| COMMENT | National Cancer Institute, Cancer Genome Anatomy Project | |
| | Tumor Gene Index | |
| | Unpublished (1997) | |
| | Contact: Robert Strausberg, Ph.D. | |
| | Email: cgapbs-r@mail.nih.gov | |
| | Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David | |
| | Ph.D., Gerald Marti, M.D. | |
| | CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fa | |
| | Bonaldo, Ph.D. | |
| | CDNA Library Arrayed by: Greg Lennon, Ph.D. | |
| | DNA Sequencing by: Washington University Genome Sequenc | |
| | Clone distribution: NCI-CGAP clone distribution informa | |
| | found through the I.M.A.G.E. Consortium/LLNL at: | |
| | www-bio.llnl.gov/bbrp/image/image.html | |
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| 1. .340 | |
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| /tissue_type="germinal center B cell" | |
| /lab_host="DH10B" | |
| /clone_lib="NCI_CGAP_GCB1" | |
| /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st site was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, CD22+, CD23+, CD24+, CD45RO+, CD45RA-), Dr. David Baltimore (NCI) and Dr. Gerald Marti (CBER). cDNA synthesized with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAATGGGAGCGCGCTCATTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI and Not I (Pharmacia), digested with Not I and cloned into pT7T3 (Pharmacia), sites of the modified pT7T3 vector. 1st round of normalization, and was constructed by Bento Soares and M. Fatima Bonal. | |

| | | | | |
|---------------------------|--------|--|-----------|-------------|
| ORIGIN | | | | |
| Query Match | 7.8%; | Score 316.4; | DB 9; | Length 340; |
| Best Local Similarity | 99.1%; | Pred. No. 2.1e-29; | | |
| Matches 339; Conservative | 0; | Mismatches 1; | Indels 2; | |
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| Db | 340 | TCACCTTCCCCACAGG-TGGCGCTCGGCTCCACCCCGAGGGCCAGCTTTTCTCTCACG | | |

11:43:36 2004

us-09-424-686f-1.rst

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April 21, 2004, 23:41:35
ecs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ein search, using sw model

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(without alignments)
3634.588 Million cell updates/sec

S-09-424-686F-2
961
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LOSUM62

apop 10.0 , Gapext 0.5

586107 seqs, 282547505 residues

its satisfying chosen parameters: 1586107

ngth: 0
ngth: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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: Geneseqp1990s: *
: Geneseqp2000s: *
: Geneseqp2001s: *
: Geneseqp2002s: *
: Geneseqp2003as: *
: Geneseqp2003bs: *
: Geneseqp2004s: *

s the number of results predicted by chance to have a
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SUMMARIES

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| 00.0 | 1132 | 2 | AAW43621 | | Aay43621 A human t |
| 00.0 | 1132 | 2 | AAW26580 | | Aay26580 Human tel |
| 00.0 | 1132 | 4 | AAW64859 | | Aag64859 Heart mus |
| 00.0 | 1132 | 4 | AAW64329 | | Aag64329 Human pro |
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| 00.0 | 1154 | 2 | AAW61350 | | Aaw61350 Human tel |
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| 40 | 5004 | 83.9 | 948 | 2 | AAW00648 | Aay00648 F |
| 41 | 4932 | 82.7 | 936 | 2 | AAW00642 | Aay00642 F |
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ALIGNMENTS

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DT 13-AUG-1998 (first entry)
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KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; F
cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harle
Andrews WH;
XX
DR WPI; 1998-171633/16.
DR N-PSDB; AAV22379.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and
variants - are useful in the diagnosis, prognosis and treatment
proliferation conditions especially cancer and ageing.
XX
PS Claim 3; Fig 17; 387pp; English.
XX
CC The present sequence represents human telomerase reverse transcr
(hTERT), which is a ribonucleoprotein. The present invention also
describes the following methods: (A) determining whether a test

For of hTERT, by detecting the change in hTERT recombinant polynucleotide, on administration of the compound; (B) a recombinant telomerase by contacting a protein preparation a telomerase RNA component; (C) detection of the hTERT RNA or a sample by binding a relevant probe to the sample and the complex formed or in the case of RNA detection, amplifying and correlating the presence of complex or amplification a presence of hTERT in the sample; and (D) increasing the on of a vertebrate cell by increasing hTERT expression; and (E) an agent that causes an increase in cell vertebrate cell on to create a medicament that inhibits ageing. A protein of hTERT and the polynucleotide encoding hTERT can be used in cure of medicaments for inhibiting the effect of ageing or bitors of telomerase activity can be used to treat conditions sociated with high telomerase activity. A protein preparation also be used in the new methods

12 AA;

100.0%; Score 5961; DB 2; Length 1132;

ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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APRPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLKRRPR 240

APPERTPVGQSWAHPGTRGSPDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 300
APPERTPVGQSWAHPGTRGSPDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 300

AHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSLRPSLTGARRL 360
AHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSLRPSLTGARRL 360

ATIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
ATIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

AGVCAREKPGQSWAAPEEEDTPRRLLVQLLRQHSPPQVYGFVACILRLRPPGLWGS 480
AGVCAREKPGQSWAAPEEEDTPRRLLVQLLRQHSPPQVYGFVACILRLRPPGLWGS 480

AVERRFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
AVERRFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

KFLHWMLSVVVVVVELLSFFVVTETTFOKNRLFYRKSWWSKLQSIGIRQHLKRVQVRE 600
KFLHWMLSVVVVVVELLSFFVVTETTFOKNRLFYRKSWWSKLQSIGIRQHLKRVQVRE 600

SAEVRQHRREARPALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
SAEVRQHRREARPALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660

SVLNYERARRPGLLGASVGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
SVLNYERARRPGLLGASVGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720

QRLTEVIAASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTDLQPYMRQFVAHL 780
QRLTEVIAASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTDLQPYMRQFVAHL 780

Db 721 PQRLTEVIAASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTDLQPYMR
Qy 781 QETSPLRDAAVVEIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQG
Db 781 QETSPLRDAAVVEIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQG
Qy 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEY
Db 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEY
Qy 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSI
Db 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSI
Qy 961 NRGFKAGRNMRRLFGVLRKCHSLFELDLQVNSLQTVCTNIYKILLQAYRFHA
Db 961 NRGFKAGRNMRRLFGVLRKCHSLFELDLQVNSLQTVCTNIYKILLQAYRFHA
Qy 1021 FHQQVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCI
Db 1021 FHQQVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCI
Qy 1081 KLTRHRVTYVPLLGSLRTAQTSRKLPGTTLTALEAAANPALPSDFKTILD 1
Db 1081 KLTRHRVTYVPLLGSLRTAQTSRKLPGTTLTALEAAANPALPSDFKTILD 1

RESULT 2

AAW90251

ID AAW90251 standard; protein; 1132 AA.

XX AAW90251;

XX 24-MAY-1999 (first entry)

XX Human catalytic telomerase sub-unit protein.

XX Human; catalytic telomerase subunit; therapy; diagnosis; hTC; a; modulator; treatment; inhibit; cellular disorder; death; defect ageing; antisense; neoplastic cell; telomerase-related condition; tumour cell.

XX Homo sapiens.

XX WO9859040-A2.

XX 30-DEC-1998.

XX 09-JUN-1998; 98WO-EP003468.

XX 20-JUN-1997; 97DE-01026329.

XX 26-MAR-1998; 98DE-01013274.

XX 14-APR-1998; 98DE-01016496.

XX (FARB) BAYER AG.

XX Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;

XX WPI; 1999-081276/07.

XX N-PSDB; AAV72117.

XX New catalytically active subunit of human telomerase - used in

XX modulation of telomerase activity, particularly for treating ca

XX ageing.

XX Claim 2; Fig 2; 76pp; German.

XX This sequence represents a novel human catalytic telomerase sub

XX (hTC). This protein can be used in screening assays to identify

XX modulators of telomerase and to treat or inhibit cellular disor

XX death, defects and/or other pathological processes involving te

XX particularly cancer and ageing (also suitable for this are agent

XX stimulate, inhibit or mimic the activity of the subunit). Antis

s inhibit telomerase action (by binding to specific mRNA), in neoplastic cells and may be expressed in vivo. Antibodies s of the protein, used as probes or primers, are used to omerase-related conditions (especially neoplasia) by (i) normal levels of the subunit protein in body fluids or ii) by measuring the amount of the encoding nucleic acid. f the nucleic acid encoding the subunit mRNA is confined to , in contrast to the ubiquitous expression of the telomerase

2 AA;
100.0%; Score 5961; DB 2; Length 1132;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQGRDPAAFRALVAQCLVCVPW 60
APRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQGRDPAAFRALVAQCLVCVPW 60
PPPAAPSFRQVSKELVARVLQRLCERGAKNVLAFGFALLDGARGPPEAFTTSVR 120
PPPAAPSFRQVSKELVARVLQRLCERGAKNVLAFGFALLDGARGPPEAFTTSVR 120
PNTVTDALRSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180
PNTVTDALRSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180
ARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKPRR 240
ARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKPRR 240
PEPERTPVGGQSWAHPGRTGSDRGFCVSPARPAEATSLEGALSCTRHSHPVG 300
PEPERTPVGGQSWAHPGRTGSDRGFCVSPARPAEATSLEGALSCTRHSHPVG 300
HAGPPSTSRPPRWDTPCPVYAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
HAGPPSTSRPPRWDTPCPVYAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
IFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
IFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
GVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLLVPPGLMGS 480
GVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLLVPPGLMGS 480
ERRFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRLEEI 540
ERRFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRLEEI 540
FLHWMMSVYVVELLRSEFFVYTTETTFQKNRLLFFYRKSVMKLSQSIGIRQHLKRVLRE 600
FLHWMMSVYVVELLRSEFFVYTTETTFQKNRLLFFYRKSVMKLSQSIGIRQHLKRVLRE 600
AEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTERREKRAERLTSRVKA 660
AEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTERREKRAERLTSRVKA 660
VLNYERARRPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
VLNYERARRPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
RLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
RLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
SPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQGSILSTL 840
SPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQGSILSTL 840
LCYGDWENKLFAGIRRDGULLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Db 841 LCSLCYGDWENKLFAGIRRDGULLRLVDDFLVTPHLTHAKTFLRTLVRGVPEY
Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIH
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIH
Qy 961 NRGFKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHAC
Db 961 NRGFKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHAC
Qy 1021 FHQOVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCE
Db 1021 FHQOVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCE
Qy 1081 KLTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFKTILD 11
Db 1081 KLTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFKTILD 11

RESULT 3
AAY28881
ID AAY28881 standard; protein; 1132 AA.
XX AAY28881;
AC AAY28881;
XX 17-JAN-2000 (first entry)
DT 17-JAN-2000 (first entry)
XX Human telomerase reverse transcriptase protein.
DE Human telomerase reverse transcriptase protein; hTERT; telomerase
XX catalytic protein component; cell proliferative capacity; DNA p
KW telomerase substrate; telomeric DNA synthesis; cell immortality;
KW neoplastic phenotype; diagnostic application; prognostic applica
KW telomerase related condition; cancer; therapeutic agent;
KW telomerase expression; telomerase activity.

XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 608 /note= "Corresponds to cac codon"
FT
XX
PN WO9950279-A1.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007160.
XX
PR 31-MAR-1998; 98US-00052919.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harle
PI Andrews WH;
XX
DR WPI; 1999-610834/52.
DR N-PSDB; AAZ08150.
XX

PT Antisense polynucleotides for human telomerase reverse transcrip
PT for diagnosing or treating cancer.
XX
PS Claim 2; Fig 2; 31pp; English.
XX
CC The present sequence is human telomerase reverse transcriptase p
CC This is the catalytic protein component of telomerase and is als
CC referred to as hEST2. hTERT has the ability to extend a DNA prime
CC functions as a telomerase substrate for telomeric DNA synthesis.
CC correlates with cell proliferative capacity, cell immortality, a
CC development of a neoplastic phenotype. Human TRT antisense
CC oligonucleotides are useful for diagnostic or prognostic applica
CC telomerase related conditions, including cancer. They are also u

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RPRCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
RPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAFTTSVR 120
RPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAFTTSVR 120
LPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCAFLVLAFCAYQVCGPPLYQLGA 180
LPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCAFLVLAFCAYQVCGPPLYQLGA 180
JAPPPPHASGPPRRRLGGERAWNHSVREAGVPLGAPGARRRGGSSASRLDLPKRPRR 240
JAPPPPHASGPPRRRLGGERAWNHSVREAGVPLGAPGARRRGGSSASRLDLPKRPRR 240
APEPERTVPGQSWAHGTRGSDRGFCVVSAPPAEATSLEGALSCTRSHSPSVG 300
APEPERTVPGQSWAHGTRGSDRGFCVVSAPPAEATSLEGALSCTRSHSPSVG 300
IHAGPPSTSRPPRWDTPCPPVYAETKHFLLYSYSGDKEQLRPSFLLSRLPSLTGARRL 360
IHAGPPSTSRPPRWDTPCPPVYAETKHFLLYSYSGDKEQLRPSFLLSRLPSLTGARRL 360
TIFLGRPMMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
TIFLGRPMMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
AGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVGFVRACLRRLVPPGLWGS 480
AGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVGFVRACLRRLVPPGLWGS 480
VERRFLRNTKKFISLGKHAHKLLOELTWKMSVRDCAWLRRSPGVGCVPAEHRRLREEI 540
VERRFLRNTKKFISLGKHAHKLLOELTWKMSVRDCAWLRRSPGVGCVPAEHRRLREEI 540
CFHLWLMSVYVVELLSRFFYVTTTTFQKNRLEFFYRKSWSKLSQSIGIRQHLKRVQLRE 600
CFHLWLMSVYVVELLSRFFYVTTTTFQKNRLEFFYRKSWSKLSQSIGIRQHLKRVQLRE 600
ZAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRKA 660
ZAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRKA 660
VLNYERARRPGLLGASVGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
VLNYERARRPGLLGASVGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
RLTEVIASIIKQNTCYVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
RLTEVIASIIKQNTCYVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
SPLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
SPLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
LCYGDMMENKLFAGIRRDGLLLRLVDDELLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
LCYGDMMENKLFAGIRRDGLLLRLVDDELLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
VNFVPEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
VNFVPEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
FKAGRNMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
FKAGRNMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLGLSLRTAQQLSRKLPCTTLTALEAAANPALPSDFKTILD 1132
|||||

Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPCTTLTALEAAANPALPSDFKTILD 1
RESULT 5
AA43621
ID AAY43621 standard; protein; 1132 AA.
XX
AC AAY43621;
XX
DT 26-JAN-2000 (first entry)
XX
DE A human telomerase reverse transcriptase (TRT) polypeptide.
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte acti
KW dendritic cell; telomerase activity; cancer cell; proliferating di
KW immunological destruction; telomerase; cancer; proliferation di
XX
OS Homo sapiens.
XX
PN WO9950392-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US006898.
XX
PR 31-MAR-1998; 98US-0112006P.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
DR WPI; 1999-610845/52.
DR N-PSDB; AAZ30154.
XX
PT Eliciting an in vivo immune response for prevention and treatme
PT cancers.
XX
PS Claim 3; Fig 1; 26pp; English.
XX
CC The present sequence represents a human telomerase reverse tran
CC (TRT) polypeptide. The protein is used in the method of the inv
CC The specification describes a method for activating a T lymphoc
CC comprising contacting the T lymphocyte with a dendritic cell th
CC expresses a TRT peptide in the context of a MHC class I or MHC
CC molecule. The protein causes induction of an in vivo immunologi
CC response to telomerase activity. Cancer cells are characterized
CC expression of endogenous TRT gene and the presence of detectabl
CC telomerase activity. Therefore, by eliciting a specific immune
CC to TRT or to TRT-expressing cells, it is possible to selectivel
CC proliferating cells for immunological destruction. The method i
CC eliciting an in vivo immune response to telomerase by activating
CC lymphocyte, and is useful for prevention and treatment of cance
CC other proliferation diseases/conditions
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPRAPCRRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQCI
Db 1 MPRAPCRRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQCI
QY 61 DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAF
Db 61 DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAF
QY 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCAFLVLAFCAYQVCGPPI
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCAFLVLAFCAYQVCGPPI
QY 181 ATQARPPPHASGPPRRRLGGERAWNHSVREAGVPLGAPGARRRGGSSASRLPLE

QARPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRRGGSSASRSLLPLPKRRR 240
APEPERTVQGSGWAHPGRTGRGSDRGFCVWSPARPAEEATSLEGALSGTRHSHPSVG 300
APEPERTVQGSGWAHPGRTGRGSDRGFCVWSPARPAEEATSLEGALSGTRHSHPSVG 300
HHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSRLPSLTGARRL 360
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TIFLSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCHPLRAAVT 420
TIFLSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCHPLRAAVT 420
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NERRFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
KFLHWMMSVYVVELLRSFFVYTTTFQKNRLLFFYKRSVWSKLSIGIRQHLLKRVQLRE 600
KFLHWMMSVYVVELLRSFFVYTTTFQKNRLLFFYKRSVWSKLSIGIRQHLLKRVQLRE 600
EAEVRQHREARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
EAEVRQHREARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
SVLNYERARRPGLLGASVGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
SVLNYERARRPGLLGASVGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
DRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
DRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
ISPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHVAIRGKSYVQCQGIPOGSILSTL 840
ISPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHVAIRGKSYVQCQGIPOGSILSTL 840
3LCYGD MENKLFAGIRRDGLLLRLVDLFLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
3LCYGD MENKLFAGIRRDGLLLRLVDLFLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
TVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASLTF 960
TVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASLTF 960
3FKAGRNMRRLKFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
3FKAGRNMRRLKFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QVWKNTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QVWKNTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
RHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

undard; protein; 1132 AA.

(first entry)

rase reverse transcriptase (hTERT) enzyme.

XX Telomerase reverse transcriptase; TERT; mouse; telomere length
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
XX Homo sapiens.
XX WO9927113-A1.
XX 03-JUN-1999.
XX 25-NOV-1998; 98WO-US025211.
XX 26-NOV-1997; 97US-00979742.
XX 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins
XX nucleic acids.
XX Disclosure; Fig 3; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase
XX enzyme. Compositions containing mTERT can be used in telomere
XX assays. Isolated mTERT is useful as an immunogen for the produc
XX monoclonal or polyclonal antibodies. The method is useful for a
XX the degree of purification and identification of new mTERT spec
XX as an mTERT allele, homolog or isoform, or to screen for modula
XX (antagonists and agonists) of telomerase-mediated DNA replicati
XX Antagonists and agonists of mTERT can be used to modify the act
XX other telomerase enzymes such as human TERT (hTERT). The presen
XX represents a human TERT enzyme

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPCRCAVRSLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQC
Db 1 MPRAPCRCAVRSLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQC
QY 61 DARPPPAAPSFQVSCLELVARVLQRCERGAKNVLAFFGALLDARGGPPPEA
Db 61 DARPPPAAPSFQVSCLELVARVLQRCERGAKNVLAFFGALLDARGGPPPEA
QY 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
QY 181 ATQARPPPHASGPRRRRLGCERAWNSVREAGVPLGLPAGARRRGGSSASRSLLPL
Db 181 ATQARPPPHASGPRRRRLGCERAWNSVREAGVPLGLPAGARRRGGSSASRSLLPL
QY 241 GAAPERTPVQGSWAHPGRTGRGSDRGFCVWSPARPAEEATSLEGALSGTRH
Db 241 GAAPERTPVQGSWAHPGRTGRGSDRGFCVWSPARPAEEATSLEGALSGTRH
QY 301 RQHEAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSRLPSLT
Db 301 RQHEAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSRLPSLT
QY 361 VETIFLSRPPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCHPI
Db 361 VETIFLSRPPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCHPI
QY 421 PAAGVCAREKPGQSVAAPEEEDTTPRRLVQLLRQHSSPWQVYGFVRACLRLRVP

RLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780
RLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780
ESPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPIQGSILSTL 840
ESPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPIQGSILSTL 840
LCYGDMDENKLFAGIRRDGLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
LCYGDMDENKLFAGIRRDGLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
VWVFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIRASLTF 960
VWVFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIRASLTF 960
FKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
FKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLLGSLRTAQTLRSKLPGTTLTALEAAANPALPSDEKTLTD 1132
RHRVTYVPLLGSLRTAQTLRSKLPGTTLTALEAAANPALPSDEKTLTD 1132

undard; protein; 1132 AA.

(first entry)

n #2.

; cardiant; cell differentiating agent; bone marrow;
; cell; heart disease; human.

A1.

2000WO-JP001148.

99JP-00372826.

A HAKKO KOGYO KK.

Hata J, Fukuda K, Ogawa S, Sakurada K;

8252/44.
9601.

ne marrow-originated cells capable of differentiating into
cells, applicable as remedies for various heart diseases
with damaged heart muscle accompanying degeneration.

Page 128-134; 158pp; Japanese.

invention relates to cells isolated from bone marrow, which
of at least differentiating into heart muscle cells. The
plicable as remedies for various heart diseases particularly
heart muscle accompanying degeneration. The present sequence
illustrate the present invention

2 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQC
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQC
QY 61 DARPPPAAPSFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEA
Db 61 DARPPPAAPSFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEA
QY 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
Db 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
QY 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRRGGASRSRLPL
Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRRGGASRSRLPL
QY 241 GAAPERTPVQGSWAHPGRTRGSDRGFCVVSPPARPAEEATSLGALSSTRH
Db 241 GAAPERTPVQGSWAHPGRTRGSDRGFCVVSPPARPAEEATSLGALSSTRH
QY 301 RQHAGPPSTSRPPRPWDTPCPVYAETKHFLYSSGDKQLRPSFLLSSLRPSL
Db 301 RQHAGPPSTSRPPRPWDTPCPVYAETKHFLYSSGDKQLRPSFLLSSLRPSL
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVQLLRHSSPWQVYGFVRACLRRLVPI
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVQLLRHSSPWQVYGFVRACLRRLVPI
QY 481 RHNERFLRNTKFKISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHF
Db 481 RHNERFLRNTKFKISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHF
QY 541 LAKFLHLMMSVYVVELLRSSFYVTTTFFQXNRLFFFYKSVWSKLQSIGIRQHLKF
Db 541 LAKFLHLMMSVYVVELLRSSFYVTTTFFQXNRLFFFYKSVWSKLQSIGIRQHLKF
QY 601 LSEAEVROHREARPALLTSRLRPIPKPDGLRPIVNMMDYVVGARTFRREKRAERLI
Db 601 LSEAEVROHREARPALLTSRLRPIPKPDGLRPIVNMMDYVVGARTFRREKRAERLI
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELYFVKVDVTG
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELYFVKVDVTG
QY 721 PQDRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQ
Db 721 PQDRLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQ
QY 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGS
Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGS
QY 841 LCSLCYGDMDENKLFAGIRRDGLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEYG
Db 841 LCSLCYGDMDENKLFAGIRRDGLLRLVDDDFLLVTPHLTHAKTFLRTLVRGVPEYG
QY 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIR
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIR
QY 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHAC
Db 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHAC

QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLIGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
RHRVTYVPLIGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

standard; protein; 1132 AA.

(first entry)

rase protein sequence SEQ ID NO:31.

ion; heart muscle cell; cytokine; transcription factor;
n; surface antigen; heart disease; cardiomyocyte;
umbilical blood cell; heart muscle degeneration;
nfraction.

Al.

2000WO-JP007741.

99JP-00372826.

2000WO-JP001148.

A HAKKO KOGYO KK.

Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;

5655/45.
4366.

e of differentiating into cardiomyocytes and originating in
or umbilical blood cells for study of cardiomyocyte
ion and treatment of heart disease.

age 137-141; 187pp; Japanese.

invention describes cells originating in bone marrow or
ood cells which are capable of differentiating into
as. Also described are: (1) cardiomyocytes produced by the
ion of the cells; (2) a method for carrying out the
ion into cardiomyocytes, regulated by a promotional and/or
actor; (3) a method for the differentiation of the cells into
ther than cardiomyocytes; (4) drug compositions promoting the
heart muscle and regeneration of heart tissue which contain
5) a method for the production of antibodies which recognise
specially antibodies which recognise a surface antigen on the
method for screening factors which promote the proliferation
; (7) a method for immortalising the cells by expressing
a them; (8) drug compositions for the treatment of heart
a contain the immortalised cells; and (9) cell-free
from the culture of the cells and its use in promoting their
ion into cardiomyocytes. The cells are used in the treatment
involving heart muscle degeneration, such as myocardial
nd in the study of cardiomyocyte differentiation. AAH44351 to
AAB99915 to AAB99935 represent sequences used in the
ion of the present invention

; AA;

100.0%; Score 5961; DB 4; Length 1132;

| | | Best Local Similarity 100.0%; Pred. No. 0; | | | |
|----|------|---|-------------------------|------------------------------|-------------|
| | | Matches 1132; Conservative 0; Mismatches 0; Indels 0; | | | |
| QY | 1 | MPRAPRCRAVRSLLRSHYREVLP | PLATFVRRLGPOGWRLVQRGDP | AAAFRALVAQC | |
| Db | 1 | MPRAPRCRAVRSLLRSHYREVLP | PLATFVRRLGPOGWRLVQRGDP | AAAFRALVAQC | |
| QY | 61 | DARPPAAPSFQVSCCLKELVARV | LQRLCERGAKNVLAFGFALLDGA | RGGPPEA | |
| Db | 61 | DARPPAAPSFQVSCCLKELVARV | LQRLCERGAKNVLAFGFALLDGA | RGGPPEA | |
| QY | 121 | SYLPNTVTDALRGSGAWGLLRV | GDDVLVHLLARCALFVLVAPSC | AYQVCGPPI | |
| Db | 121 | SYLPNTVTDALRGSGAWGLLRV | GDDVLVHLLARCALFVLVAPSC | AYQVCGPPI | |
| QY | 181 | ATQARPPPHASGPRRLGCERAW | NSVREAGVPLGLPAGARRRGG | SASRSLPLI | |
| Db | 181 | ATQARPPPHASGPRRLGCERAW | NSVREAGVPLGLPAGARRRGG | SASRSLPLI | |
| QY | 241 | GAAPERTPVQGSWAHPGTRGPD | SRGFCVVSPPARPAEATSLEGA | LSGTRHK | |
| Db | 241 | GAAPERTPVQGSWAHPGTRGPD | SRGFCVVSPPARPAEATSLEGA | LSGTRHK | |
| QY | 301 | ROHAGPPSTSRPPRPWDTPCP | PVYAEKHFLYSSGDKQLRPS | FLLSSLRPSLJ | |
| Db | 301 | ROHAGPPSTSRPPRPWDTPCP | PVYAEKHFLYSSGDKQLRPS | FLLSSLRPSLJ | |
| QY | 361 | VETIFLGSRPWMPGT | PRRLPRLPQRYWQMRPLFLE | LGNHAQC | PYGVLKTHCPI |
| Db | 361 | VETIFLGSRPWMPGT | PRRLPRLPQRYWQMRPLFLE | LGNHAQC | PYGVLKTHCPI |
| QY | 421 | PAAGVCAREKPGQSVAAPEED | TPRRLVQLLRHSSPWQVGFV | RACLRRLVPI | |
| Db | 421 | PAAGVCAREKPGQSVAAPEED | TPRRLVQLLRHSSPWQVGFV | RACLRRLVPI | |
| QY | 481 | RHNERRFLRNTKKFISLGKHA | KLQELTWKMSVRDCAWLRSP | GVGCVPAAEHF | |
| Db | 481 | RHNERRFLRNTKKFISLGKHA | KLQELTWKMSVRDCAWLRSP | GVGCVPAAEHF | |
| QY | 541 | LAKFLHMLMSVYVVELLR | SFFVTETTFQKNRFFYRK | SVWSKLQSIGIRQHLKR | |
| Db | 541 | LAKFLHMLMSVYVVELLR | SFFVTETTFQKNRFFYRK | SVWSKLQSIGIRQHLKR | |
| QY | 601 | LSEAEVRQHREAR | PALLTSRLRFIPKPDGLR | PIVNM DYVVGARTFRREKRAERLT | |
| Db | 601 | LSEAEVRQHREAR | PALLTSRLRFIPKPDGLR | PIVNM DYVVGARTFRREKRAERLT | |
| QY | 661 | LFSVLNYERARRPGL | LGASVLGLDDIHR | AWRTFVLVRVRAQDPPPELYFVKVDVTG | |
| Db | 661 | LFSVLNYERARRPGL | LGASVLGLDDIHR | AWRTFVLVRVRAQDPPPELYFVKVDVTG | |
| QY | 721 | PQDRLTEVIASIIKPQNTY | CVRRYAVVQKAHGHVRKAFKSHV | STLTDLPYMRQ | |
| Db | 721 | PQDRLTEVIASIIKPQNTY | CVRRYAVVQKAHGHVRKAFKSHV | STLTDLPYMRQ | |
| QY | 781 | QETSPLRDAVVIQSSSLNEA | SSGLFDVFLRFMCHHAVRIRK | SVYVQCQIPQGS | |
| Db | 781 | QETSPLRDAVVIQSSSLNEA | SSGLFDVFLRFMCHHAVRIRK | SVYVQCQIPQGS | |
| QY | 841 | LCSLCYGDMENKLFAGIR | RDGLLRVDDFLVTPHLTHAKT | FLRTLVRGVPYEG | |
| Db | 841 | LCSLCYGDMENKLFAGIR | RDGLLRVDDFLVTPHLTHAKT | FLRTLVRGVPYEG | |
| QY | 901 | RKTVVNFVEDEALGGTAF | VQMPAHGLFPWCGLLDDTRT | LEVQSDYSSYARTSIR | |
| Db | 901 | RKTVVNFVEDEALGGTAF | VQMPAHGLFPWCGLLDDTRT | LEVQSDYSSYARTSIR | |
| QY | 961 | NRGFKAGRNMRKLF | GVLRKCHSLFLDLQVNSLQ | TCTNIYKILLQAYRFHAC | |
| Db | 961 | NRGFKAGRNMRKLF | GVLRKCHSLFLDLQVNSLQ | TCTNIYKILLQAYRFHAC | |
| QY | 1021 | FHQQVWKNPTFFLR | VISDTASLCYSILKAKNAGMS | LGAKGAGPLPSEAVQWLCH | |

QQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

TRHRVTYVPLLSRLTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
|||||
TRHRVTYVPLLSRLTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

andard; protein; 1132 AA.

(first entry)

rase reverse transcriptase.

reverse transcriptase; hTERT; human; cancer; tumour;
lymphocyte; major histocompatibility complex;
yte antigen; HLA-A2.1; vaccine.

3.

Location/Qualifiers

13. .21 /note= "HLA-A2.1 binding motif"
23. .31 /note= "HLA-A2.1 binding motif"
76. .84 /note= "HLA-A2.1 binding motif"
96. .104 /note= "HLA-A2.1 binding motif"
140. .148 /note= "HLA-A2.1 binding motif"
152. .160 /note= "HLA-A2.1 binding motif"
346. .354 /note= "HLA-A2.1 binding motif"
353. .361 /note= "HLA-A2.1 binding motif"
371. .379 /note= "HLA-A2.1 binding motif"
388. .396 /note= "HLA-A2.1 binding motif"
407. .415 /note= "HLA-A2.1 binding motif"
487. .495 /note= "HLA-A2.1 binding motif"
540. .548 /label= p540
/note= "HLA-A2.1 binding motif"
548. .556 /note= "HLA-A2.1 binding motif"
555. .563 /note= "HLA-A2.1 binding motif"
572. .580 /note= "HLA-A2.1 binding motif"
705. .713 /note= "HLA-A2.1 binding motif"
724. .732 /note= "HLA-A2.1 binding motif"
772. .780 /note= "HLA-A2.1 binding motif"
797. .805 /note= "HLA-A2.1 binding motif"
812. .820 /note= "HLA-A2.1 binding motif"
836. .844 /note= "HLA-A2.1 binding motif"
863. .871 /note= "HLA-A2.1 binding motif"
865. .873 /note= "HLA-A2.1 binding motif"
/label= p865

Peptide /note= "HLA-A2.1 binding motif"
883. .891
Peptide /note= "HLA-A2.1 binding motif"
926. .934
Peptide /note= "HLA-A2.1 binding motif"
934. .942
Peptide /note= "HLA-A2.1 binding motif"
969. .977
Peptide /note= "HLA-A2.1 binding motif"
988. .996
Peptide /note= "HLA-A2.1 binding motif"
1072. .1080
Peptide /note= "HLA-A2.1 binding motif"
1079. .1087
Peptide /note= "HLA-A2.1 binding motif"
1095. .1103
Peptide /note= "HLA-A2.1 binding motif"
1122. .1130
Peptide /note= "HLA-A2.1 binding motif"

WO200160391-A1.

23-AUG-2001.

15-FEB-2001; 2001WO-US005143.

15-FEB-2000; 2000US-0182685P.

15-FEB-2001; 2001US-00182685.

(REGC) UNIV CALIFORNIA.

Zanetti M;

WPI; 2001-536552/59.

Vaccine for initiating and enhancing a cytotoxic T lymphocyte re
for treating cancers or tumors or for inducing immune response a
tumors, comprises a telomerase reverse transcriptase peptide.

Disclosure; Fig 5; 52pp; English.

The present sequence is that of human telomerase reverse transcr
(hTERT). The sequence was analysed for 9-mer peptide sequences cc
known binding motifs for the human leukocyte antigen HLA-A2.1 mc
From an initial panel of about 30 candidate peptides, 2 sequence
denoted p540 (see AAB82772) and p865 (see AAB82773), were examir
majority of healthy individuals as well as patients with prostat
immunised in vitro against these 2 HLA-A2.1 restricted peptides
hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients
specifically lysed a variety of HLA-A2+ cancer cell lines such a
prostate, breast, colon, lung and melanoma, demonstrating immunc
recognition of endogenously-processed hTERT peptides. In vivo imm
of HLA-A2.1 transgenic mice generated a specific CTL response ag
both hTERT peptides. The induction of CTL responses in vitro and
and the susceptibility to lysis of tumour cells of various origi
hTERT CTL suggest that hTERT could serve as a universal cancer vac
humans. Thus, a claimed universal vaccine for treating tumours o
origin comprises at least 1 hTERT peptide in an amount effective
initiating and enhancing a CTL response against cancer cells. Th
is 7-15 amino acid residues in length and may be modified to enh
binding to the major histocompatibility complex. Also claimed is
for inducing and enhancing a CTL response against cancer cells,
harvesting blood leucocytes, pulsing with hTERT, and contacting c
cells with the pulsed leucocytes. A method for targeting CTL to
cells is also claimed, and involves administering a hTERT peptide
mammal, especially a cancer patient

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

RAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVORGDPAAFRALVAQCLVCPW 60
RAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVORGDPAAFRALVAQCLVCPW 60
RPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
RPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
LPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
LPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
JAPPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRGGASRSLSLPKRRPR 240
JAPPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRGGASRSLSLPKRRPR 240
APEPERTVPGQSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSCTRHSHPVSG 300
APEPERTVPGQSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSCTRHSHPVSG 300
IHAGPPSTSRPPRWDTPCPPVYAEKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
IHAGPPSTSRPPRWDTPCPPVYAEKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
IFLGSRPWMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
IFLGSRPWMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
GVCAAREKPOGSAAPAEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
GVCAAREKPOGSAAPAEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
IERRFLRNTKFIISLGKHAHKLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
IERRFLRNTKFIISLGKHAHKLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
FLHWMMSVVVVELLRSPFYVTETTFQKNRLEFFYKRSVMSKLSQISGIRQHLKRVOLRE 600
FLHWMMSVVVVELLRSPFYVTETTFQKNRLEFFYKRSVMSKLSQISGIRQHLKRVOLRE 600
AEVROHREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTFREKRAERLTSRVKA 660
AEVROHREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTFREKRAERLTSRVKA 660
VLNYERARRPGLLGASVGLDLDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
VLNYERARRPGLLGASVGLDLDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
RLTEVIASIIKQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
RLTEVIASIIKQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
SPLRDVAVIEQSSSLNEASSGLEDFVLRFMCHHAVIRGKSVYQCQGIPOQSILSTL 840
SPLRDVAVIEQSSSLNEASSGLEDFVLRFMCHHAVIRGKSVYQCQGIPOQSILSTL 840
LCYGDMMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVMNL 900
LCYGDMMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVMNL 900
VYNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIRASLTF 960
VYNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIRASLTF 960
FKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVQLP 1020
FKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVQLP 1020
QVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

Db 1081 KLTRHRVTYVPLLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1
RESULT 11
AAE29226
ID AAE29226 standard; protein; 1132 AA.
XX AAE29226;
AC
XX
DT 27-JAN-2003 (first entry)
XX Human telomerase reverse transcriptase (TERT).
DE Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3
XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; en
KW telomerase reverse transcriptase.
KW Homo sapiens.
XX
OS WO200274948-A2.
XX
PN 26-SEP-2002.
XX
PD 21-MAR-2002; 2002WO-CA000378.
XX
PF 21-MAR-2001; 2001US-0277811P.
XX
PR (GERO-) GERON CORP.
XX Denning C, Clark AJ, Schiff JM;
PI WPI; 2002-759895/82.
XX N-PSDB; AAD46821.
XX Mammalian cells, useful for producing animal tissues with carbo
PT antigens that are compatible for transplantation into human pat
PT
XX Disclosure; Page 34; 71pp; English.
XX The invention relates to animal tissues with carbohydrate anti
CC are compatible for transplantation into human patients. The mam
CC cell is inactivated homozygously for expression of alpha(1,3)ga
CC transferase (alpha1,3GT) gene and comprises a transgene for alpi
CC fucosyltransferase (alpha1,2FT). It is useful for producing ani
CC with carbohydrate antigens that are compatible for transplantat
CC human patients. The present sequence is human telomerase revers
CC transcriptase (TERT) used in the invention
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVORGDPAAFRALVAQCI
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVORGDPAAFRALVAQCI
QY 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAF
Db 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAF
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRGGASRSLSPLP
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRGGASRSLSPLP
QY 241 GAAPEPERTVPGQSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSCTRHS

APEPRTVQGSWAHPGRTGRGSDRGFCVWSPARPAEATSLGALSCTRHSHPVG 300
HHAGPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
HHAGPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
TIFLSRPPMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
TIFLSRPPMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
AGVCAREKPGQSVAAPEEEDTTPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
AGVCAREKPGQSVAAPEEEDTTPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
NERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
NERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
KFLHWMMSVYVVELLRSFFVYTTTTFQKNRLLFFYKRSVWSKLSIGIRQHLLKRVQLRE 600
KFLHWMMSVYVVELLRSFFVYTTTTFQKNRLLFFYKRSVWSKLSIGIRQHLLKRVQLRE 600
SAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
SAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
SVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
SVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
JRLTEVIAIIKPNQYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
JRLTEVIAIIKPNQYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
TSPLRDVAVIEQSSSLNEASSGLDFVFLREMHCHAVIRGKSVYVQCQIPQGSILSTL 840
TSPLRDVAVIEQSSSLNEASSGLDFVFLREMHCHAVIRGKSVYVQCQIPQGSILSTL 840
SLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
SLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
TVNFPVEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
TVNFPVEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
IFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
IFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
QVWKNPTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
RHRVTYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132

ndard; protein; 1132 AA.

(first entry)

rase reverse transcriptase (TERT).

everse transcriptase; TERT; cytostatic; apoptosis;
inhibitor; antisense oligonucleotide; antisense technology.

XX PN WO200188198-A1.
XX PD 22-NOV-2001.
XX PF 15-MAY-2001; 2001WO-US015774.
XX PR 16-MAY-2000; 2000US-00572423.
XX PR 07-DEC-2000; 2000US-00733294.
XX (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX PI WPI; 2002-075321/10.
XX DR N-PSDB; AAS96607.
XX PT New compound targeted to nucleic acid molecule encoding telomere
PT transcriptase (TERT), which specifically hybridizes with and in
PT expression of TERT, useful for modulating apoptosis and inhibit
PT growth.
XX Disclosure; Page 100-105; 154pp; English.
CC The invention describes a compound, 8-50 nucleobases in length
CC to a nucleic acid molecule encoding human TERT (telomerase reve
CC transcriptase), where the compound specifically hybridizes with
CC inhibits the expression of TERT. A series of oligonucleotides w
CC designed to target different regions of the human TERT RNA. The
CC nucleotides in length and composed of a central gap region cons
CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' direc
CC five-nucleotide wings. The wings were composed of 2'-methoxyeth
CC MOE) nucleotides. The compounds were analysed for their effect
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain
CC (PCR). The compound is useful for inhibiting the expression of
CC cells or tissues, for treating a human having disease or condit
CC associated with TERT, for modulating apoptosis, for inhibiting
CC growth (preferably, cancer cell growth), in antisense therapy a
CC diagnostics and therapeutics. This is the amino acid sequence o
CC telomerase reverse transcriptase (TERT), described in the metho
CC invention
XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAFCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQGRDPAAFRALVAQCI
Db 1 MPRAFCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQGRDPAAFRALVAQCI
QY 61 DARPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGPPEAI
Db 61 DARPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGPPEAI
QY 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
QY 181 ATQARPPPHASGPPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGASRSRLPLF
Db 181 ATQARPPPHASGPPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGASRSRLPLF
QY 241 GAAPEPERTPVQGSWAHPGRTGRGSDRGFCVWSPARPAEATSLGALSCTRHS
Db 241 GAAPEPERTPVQGSWAHPGRTGRGSDRGFCVWSPARPAEATSLGALSCTRHS
QY 301 RQHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLT
Db 301 RQHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLT
QY 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPL

|||||
IIFLGSRPWMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
|||||
AGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
|||||
AGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
|||||
JERRFLRNTKFKISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
|||||
JERRFLRNTKFKISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
|||||
CFLHWMMSVYVVELLRSEFFVYVTTTTFQKNRLLFFYRKSWSKLSQSIGIRQHLKRVQLRE 600
|||||
CFLHWMMSVYVVELLRSEFFVYVTTTTFQKNRLLFFYRKSWSKLSQSIGIRQHLKRVQLRE 600
|||||
JAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTFRREKRAERLTSRVKA 660
|||||
JAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTFRREKRAERLTSRVKA 660
|||||
JVLNERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
|||||
JVLNERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
|||||
JRLTEVIASIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
|||||
JRLTEVIASIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
|||||
JSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCQIGIPIQSILSTL 840
|||||
JSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCQIGIPIQSILSTL 840
|||||
JLCYGDMMENKLFAGIRRDGLLLRLVDLDFLLVTPHLTHAKTFLRLVIRGVPEYGCVVNL 900
|||||
JLCYGDMMENKLFAGIRRDGLLLRLVDLDFLLVTPHLTHAKTFLRLVIRGVPEYGCVVNL 900
|||||
JVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSSYARTSIRASLTF 960
|||||
JVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSSYARTSIRASLTF 960
|||||
JFKAGNMRRKLFGLVRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
|||||
JFKAGNMRRKLFGLVRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
|||||
JQVKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
|||||
JQVKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
|||||
JRHRTYVPLLGSLRTAQTLQSLRKLPGTTLTALAANAANPALPSDFKTILD 1132
|||||
JRHRTYVPLLGSLRTAQTLQSLRKLPGTTLTALAANAANPALPSDFKTILD 1132

ndard; protein; 1132 AA.

(first entry)

rase reverse transcriptase.

erse reverse transcriptase; TERT; enzyme; RNA interference;
ering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
seive; antiinfertility; fungicide; antiparasitic;
tory; human; gene therapy.

-A2.

PF 16-OCT-2002; 2002WO-US033065.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UVRP) UNIV ROCHESTER.
XX
PI Rowley PT;
XX
DR WPI; 2003-403336/38.
DR N-PSDB; ACC58039.
XX
PT Novel double-stranded short interfering RNA having sense and an
PT nucleic acids which are complementary to each other and to targ
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX

Disclosure; Fig 4; 37pp; English.

The present sequence is the protein sequence of human telomerase
transcriptase (TERT). The invention relates to the discovery the
stranded interfering RNAs, such as short interfering RNAs (siRN
target telomerase RNA or TERT mRNA are capable of inhibiting te
activity. Inhibition of telomerase in cancer cells leads to tel
shortening, end-to-end chromosomal fusion, and apoptosis. Inter
telomerase activity can also be used for treatment of infertili
contraception or sterilisation, for immunosuppression, for treat
yeast, parasite and fungal infections, and in antiinflammatory t
As telomerase is active in a limited number of cell types, e.g.
cells, germline cells, certain stem cells of the haematopoietic
and B cells, sun-damaged skin, and proliferative cervix, most n
cells are not affected by telomerase RNA interference therapy

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCI
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCI
QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAF
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAF
QY 121 SYLPNTVTDALRGSGAWGLLRRVDDVLVHLLARCAFLVLAQCPYGVLLKTHCPL
Db 121 SYLPNTVTDALRGSGAWGLLRRVDDVLVHLLARCAFLVLAQCPYGVLLKTHCPL
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPL
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPL
QY 241 GAAPEPERTPVQGSWAHPGRTGRPSDRGFCVVSPARPAAEATSLEGALSGTRHS
Db 241 GAAPEPERTPVQGSWAHPGRTGRPSDRGFCVVSPARPAAEATSLEGALSGTRHS
QY 301 RQHAGPPSTSRPPRPWDTPCPPVYAETKHLYSSGDKEQLRPSFLLSSLRPSLT
Db 301 RQHAGPPSTSRPPRPWDTPCPPVYAETKHLYSSGDKEQLRPSFLLSSLRPSLT
QY 361 VETIFLGSRPWMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPL
Db 361 VETIFLGSRPWMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPL
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPP
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPP
QY 481 RHNERRFLRNTKFKISLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHR

AEVROHREARPAALLTSRLRIFPKPDLRPIVNDYVVGARTFRREKRAERLTSRKA 660
VLNERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
VLNERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
RLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
RLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
SPLRDVAVIEQSSSLNEASSGLEDFVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
SPLRDVAVIEQSSSLNEASSGLEDFVFLRFMCHHAVIRGKSYVQCQGIPOQSILSTL 840
LCYGMENKLFAGIRRDGGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGVVNL 900
LCYGMENKLFAGIRRDGGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGVVNL 900
VNFPEVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
VNFPEVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
FKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
FKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
RHRVTYVPLLGSLRTAQTLQRKLPGLTTLTALEAAANPALPSDFKTILD 1132
RHRVTYVPLLGSLRTAQTLQRKLPGLTTLTALEAAANPALPSDFKTILD 1132

ndard; protein; 1132 AA.

(first entry)

rase reverse transcriptase protein SEQ ID NO:2.

ase reverse transcriptase; enzyme; hTERT; chromosome 5;
atiulcer; epithelial cell migration promoter; wound;
on; skin wound; lesion; burn; surgical incision; ulcer;
all; keratinocyte; epidermal; mucosal.

a2.

2002WO-US014867.

2001US-0289903P.

J CORP.

Iu C, Harley CB;

0591/11.
2474.

for treating wounds and enhancing epithelization of a skin
prises vector encoding telomerase reverse transcriptase or
epithelial cells on a microparticle or a matrix.

page 32; 68pp; English.

The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (I) an excipient or device, or comprises telomerase epithelial cell microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnerary and antiulcer activities and can be used to promote epithelial cell migration. useful for treating a wound and enhancing epithelisation of a skin surface. The wound is especially skin wound including acute lesion as traumatic lesion, burn, or surgical incision, chronic lesion chronic venous ulcer, diabetic ulcer or compression ulcer and the is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment also in fibroblasts or endothelial cells at the site of treatment epithelial cells are especially keratinocytes. A polynucleotide TERT is useful for the preparation of a medicament for treatment wound or an epithelial surface in a human or animal. An epithelial with increased telomerase activity or increased expression of TERT useful for preparation of a medicament for the treatment of a wound human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, nose, oesophagus, stomach, or intestine. The present sequence is human TERT (hTERT), which is given in the exemplification of the invention. hTERT is located to chromosome 5

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
QY 61 DARPPPAAPSFQVSLKELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAF
Db 61 DARPPPAAPSFQVSLKELVARVLQRLCERGAKNVLAFFGALLDGGGPPPEAF
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
QY 181 ATQARPPPHASGPRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRSLPLP
Db 181 ATQARPPPHASGPRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRSLPLP
QY 241 GAAPEPERTVPGQSSWAHPGRTGRGSDRGFCVVSAPARPAEATSLGALSCTRHS
Db 241 GAAPEPERTVPGQSSWAHPGRTGRGSDRGFCVVSAPARPAEATSLGALSCTRHS
QY 301 RQHHAGPPSTSRPRPMDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLT
Db 301 RQHHAGPPSTSRPRPMDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLT
QY 361 VETIFLGSRPWMPGTTPRRLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKTHCPL
Db 361 VETIFLGSRPWMPGTTPRRLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKTHCPL
QY 421 PAAGVCAREKPGQSSVAAPPEEDTPRRLVQLLRQHSSPWQVYGFVRACLRRLVPP
Db 421 PAAGVCAREKPGQSSVAAPPEEDTPRRLVQLLRQHSSPWQVYGFVRACLRRLVPP
QY 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGVPAAEHRJ
Db 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGVPAAEHRJ
QY 541 LAKFLHMLMSVYVVELLRSFYVTTTTFQKNRLFYRKSVMKLSQSIGIRQHLKR
Db 541 LAKFLHMLMSVYVVELLRSFYVTTTTFQKNRLFYRKSVMKLSQSIGIRQHLKR
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLT
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLT

3VLNYERARRPGLLGASVLGLDDIIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
3VLNYERARRPGLLGASVLGLDDIIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
3RLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
3RLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
3SPLRDVAVIEOSSSLNEASSGLFDVFLRFMCHHAVRIRKSYVQCQGIPOGSILSTL 840
3SPLRDVAVIEOSSSLNEASSGLFDVFLRFMCHHAVRIRKSYVQCQGIPOGSILSTL 840
3LCYGDMMENKLFAGIRRDGLLLRLVDDELLVTPHLTHAKTFRLTLRGVPEYGCVVNL 900
3LCYGDMMENKLFAGIRRDGLLLRLVDDELLVTPHLTHAKTFRLTLRGVPEYGCVVNL 900
3VVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOQSDYSSYARTSIRASLTF 960
3VVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOQSDYSSYARTSIRASLTF 960
3FKAGRNMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
3FKAGRNMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
3QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
3QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
3RHRVTYVPLGLSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1132
3RHRVTYVPLGLSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1132

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us-09-424-686f-2.ra1

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ein search, using sw model

April 22, 2004, 00:12:11 ; Search time 26 Seconds
(without alignments)
2247.715 Million cell updates/sec

JS-09-424-686F-2
5961
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3LOSUM62
Gapop 10.0 , Gapext 0.5

89414 seqs, 51625971 residues

its satisfying chosen parameters: 389414

ngth: 0
ngth: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:*
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: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

as the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

| atch | Length | DB | ID | Description |
|------|--------|----|--------------------|-------------------|
| 00.0 | 1132 | 3 | US-08-851-843A-225 | Sequence 225, App |
| 00.0 | 1132 | 3 | US-08-974-549A-2 | Sequence 2, Appli |
| 00.0 | 1132 | 3 | US-08-854-050-225 | Sequence 225, App |
| 00.0 | 1132 | 4 | US-09-430-323-225 | Sequence 225, App |
| 00.0 | 1132 | 4 | US-09-128-354-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-09-675-321-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-09-052-919-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-08-912-951-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-09-402-181B-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-09-721-456-2 | Sequence 2, Appli |
| 00.0 | 1132 | 4 | US-09-953-052-2 | Sequence 2, Appli |
| 00.0 | 1154 | 3 | US-08-974-549A-611 | Sequence 611, App |
| 00.0 | 1154 | 4 | US-08-912-951-323 | Sequence 323, App |
| 00.0 | 1154 | 4 | US-09-402-181B-611 | Sequence 611, App |
| 00.0 | 1154 | 4 | US-09-721-456-611 | Sequence 611, App |
| 00.0 | 1189 | 3 | US-08-974-549A-613 | Sequence 613, App |
| 00.0 | 1189 | 4 | US-08-912-951-325 | Sequence 325, App |
| 00.0 | 1189 | 4 | US-09-402-181B-613 | Sequence 613, App |
| 00.0 | 1189 | 4 | US-09-721-456-613 | Sequence 613, App |
| 00.0 | 1200 | 3 | US-08-974-549A-612 | Sequence 612, App |
| 00.0 | 1200 | 4 | US-08-912-951-324 | Sequence 324, App |
| 00.0 | 1200 | 4 | US-09-402-181B-612 | Sequence 612, App |
| 00.0 | 1200 | 4 | US-09-721-456-612 | Sequence 612, App |
| 00.0 | 1285 | 3 | US-08-974-549A-600 | Sequence 600, App |
| 00.0 | 1285 | 4 | US-08-912-951-314 | Sequence 314, App |
| 00.0 | 1285 | 4 | US-09-402-181B-600 | Sequence 600, App |
| 00.0 | 1285 | 4 | US-09-721-456-600 | Sequence 600, App |

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| 28 | 5952 | 99.8 | 1132 | 3 | US-08-974-549A-344 | Sequence |
| 29 | 5952 | 99.8 | 1132 | 4 | US-09-402-181B-344 | Sequence |
| 30 | 5952 | 99.8 | 1132 | 4 | US-09-721-456-344 | Sequence |
| 31 | 5952 | 99.8 | 1407 | 3 | US-08-974-549A-628 | Sequence |
| 32 | 5952 | 99.8 | 1407 | 4 | US-08-912-951-334 | Sequence |
| 33 | 5952 | 99.8 | 1407 | 4 | US-09-402-181B-628 | Sequence |
| 34 | 5952 | 99.8 | 1407 | 4 | US-09-721-456-628 | Sequence |
| 35 | 4052 | 68.0 | 807 | 3 | US-08-974-549A-5 | Sequence |
| 36 | 4052 | 68.0 | 807 | 4 | US-08-912-951-5 | Sequence |
| 37 | 4052 | 68.0 | 807 | 4 | US-09-402-181B-5 | Sequence |
| 38 | 4052 | 68.0 | 807 | 4 | US-09-721-456-5 | Sequence |
| 39 | 3819.5 | 64.1 | 1003 | 3 | US-08-851-843A-217 | Sequence |
| 40 | 3819.5 | 64.1 | 1003 | 3 | US-08-974-549A-336 | Sequence |
| 41 | 3819.5 | 64.1 | 1003 | 3 | US-08-854-050-217 | Sequence |
| 42 | 3819.5 | 64.1 | 1003 | 4 | US-09-430-323-217 | Sequence |
| 43 | 3819.5 | 64.1 | 1003 | 4 | US-09-402-181B-336 | Sequence |
| 44 | 3819.5 | 64.1 | 1003 | 4 | US-09-721-456-336 | Sequence |
| 45 | 3134 | 52.6 | 622 | 4 | US-09-582-924B-12 | Sequence |

ALIGNMENTS

RESULT 1
US-08-851-843A-225
; Sequence 225, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:

ARACTERISTICS:

1132 amino acids

ino acid

linear

PE: protein

25

100.0%; Score 5961; DB 3; Length 1132;

ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEQSDYSSYARTSI

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RESULT 2

US-08-974-549A-2

; Sequence 2, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

N NUMBER: WO PCT/US97/17885
E: 01-OCT-1997
NT INFORMATION:
le, Randolph Ted
ON NUMBER: 36,429
DOCKET NUMBER: 015389-002610US
ATION INFORMATION:
(415) 576-0200
(415) 576-0300
R SEQ ID NO: 2:
ACTERISTICS:
132 amino acids
no acid
linear
E: protein

100.0%; Score 5961; DB 3; Length 1132;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 901 RKTIVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTILEVQSDYSYARTSII
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Db 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA;
QY 1021 FHQVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCH
Db 1021 FHQVWKNPTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCH
QY 1081 KLTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFKTILD 11
Db 1081 KLTRHRVTYVPLLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFKTILD 11

RESULT 3
US-08-854-050-225
; Sequence 225, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

ON NUMBER: 36,429
DOCKET NUMBER: 015389-002930US
ATION INFORMATION:
(415) 576-0200
R SEQ ID NO: 225:
RACTERISTICS:
132 amino acids
no acid
linear
E: protein
;

100.0%; Score 5961; DB 3; Length 1132;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQGDPAAFRALVAQCLVCPW 60
APRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQGDPAAFRALVAQCLVCPW 60

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ARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLKPRRR 240
ARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLKPRRR 240

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PEPERTVPGQSWAHGPRTRGPDSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300

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IFLGSRPWMCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

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VLNYERARRPGLLGASVLGLDDIHRWMTFVLVRVRAQDPPPELFPVKVDVTGAYDTI 720

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961 NRGFKAGRNMRKLFVLRRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA
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RESULT 4
US-09-430-323-225
; Sequence 225, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
;

1 100.0%; Score 5961; DB 4; Length 1132;
 2 100.0%; Pred. No. 0;
 3 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 RESULT 5
 US-09-128-354-2
 ; Sequence 2, Application US/09128354
 ; Patent No. 6337200
 ; GENERAL INFORMATION:
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Geron Corporation
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
 ; FILE REFERENCE: 015389-003310US
 ; CURRENT APPLICATION NUMBER: US/09/128,354
 ; CURRENT FILING DATE: 1998-08-03
 ; EARLIER APPLICATION NUMBER: US 08/851,843
 ; EARLIER FILING DATE: 1997-05-06
 ; EARLIER APPLICATION NUMBER: US 08/854,050
 ; EARLIER FILING DATE: 1997-05-09
 ; EARLIER APPLICATION NUMBER: US 08/911,312
 ; EARLIER FILING DATE: 1997-08-14
 ; EARLIER APPLICATION NUMBER: US 08/912,951
 ; EARLIER FILING DATE: 1997-08-14
 ; EARLIER APPLICATION NUMBER: US 08/915,503
 ; EARLIER FILING DATE: 1997-08-14
 ; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
 ; EARLIER FILING DATE: 1997-10-01
 ; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
 ; EARLIER FILING DATE: 1997-10-01
 ; EARLIER APPLICATION NUMBER: US 08/974,549
 ; EARLIER FILING DATE: 1997-11-19
 ; EARLIER APPLICATION NUMBER: US 08/974,584
 ; EARLIER FILING DATE: 1997-11-19
 ; EARLIER APPLICATION NUMBER: US 09/052,864
 ; EARLIER FILING DATE: 1998-03-31
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 US-09-128-354-2
 Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
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 Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCL
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 Db 61 DARPPAAPSPFQVSCLELVARVQLRCLCERGAQNVLAFGFALLDGCARGGPPPEAF
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 QY 241 GAAPEPERTPVGQSWAHGPRTRGSDRGFCVWSPARPAEATSLGALSCTRHS

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lication US/09675321

735

ATION:

ata, Federico C.A.

iron Corporation

ATION: Methods and Compositions for Eliciting an Immune

ATION: Response to a Telomerase Antigen

E: 015389-003500PC

ATION NUMBER: US/09/675,321

DATE: 2000-09-28

ATION NUMBER: US 60/112,006

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPQGWRLVQRGDPAAFRALVAQC
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPQGWRLVQRGDPAAFRALVAQC
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Db 61 DARPPPAAPSPROVSCIKELVARVLQRCERGAKNVLAFGFALLDGARGGPPPEA
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Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
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Db 721 PQDRLTEVIAIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMR
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Application US/09052919
i650
ATION:
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
ENTION: Antisense Compositions for Detecting and
ENTION: Inhibiting Telomerase Reverse Transcriptase
SEQUENCES: 72
ICE ADDRESS:
Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San Francisco
California
USA
1-3834
ADABLE FORM:
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
ICATION DATA:
N NUMBER: US/09/052,919
E: 31-MAR-1998
ATION: 435
ATION DATA:
N NUMBER: US 08/724,643
E: 01-OCT-1996
ATION DATA:
N NUMBER: US 08/844,419
E: 18-APR-1997
ATION DATA:
N NUMBER: US 08/846,017
E: 25-APR-1997
ATION DATA:
N NUMBER: US 08/851,843
E: 06-MAY-1997
ATION DATA:
N NUMBER: US 08/854,050
E: 09-MAY-1997
ATION DATA:
N NUMBER: US 08/911,312
E: 14-AUG-1997
ATION DATA:
N NUMBER: US 08/912,951
E: 14-AUG-1997
ATION DATA:
N NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-052-919-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLLVQRGDPAAFPALVAQC
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Publication US/08912951

1789

ATION:

Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
ENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
ENTION: THERAPEUTIC METHODS
SEQUENCES: 335
ICE ADDRESS:
Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
San Francisco
California
United States of America

ADABLE FORM:
E: Floppy disk
E: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
ICATION DATA:
ON NUMBER: US/08/912,951
E: 14-AUG-1997
ATION: 435
ATION DATA:
ON NUMBER: US 08/854,050
E: 09-MAY-1997
ATION: 435
ATION DATA:
ON NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLGPGQWRLVQRGDPAAFRALVAQCI
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLGPGQWRLVQRGDPAAFRALVAQCI
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Db 61 DARPPPAAPSFRQVSKLVARVLQRLCERGAKNVLAFGFALLDGGARGGPPEAI
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
QY 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRRGGASRSPLI
Db 181 ATQARPPPHASGPRRRRLGGERAMNHSVREAGVPLGLPAPGARRRGGASRSPLI
QY 241 GAAPERTPVQGSWAHPGRTGRSDRGFCVVSPPARPAEATSLGALSSTRH
Db 241 GAAPERTPVQGSWAHPGRTGRSDRGFCVVSPPARPAEATSLGALSSTRH
QY 301 RQHHAGFPSTSRPPRPWDTPCPVYAEKTHFLYSSGDKQLRPSFLLSSLRPSLI
Db 301 RQHHAGFPSTSRPPRPWDTPCPVYAEKTHFLYSSGDKQLRPSFLLSSLRPSLI
QY 361 VETIFLGSRPWMPGTPLRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
Db 361 VETIFLGSRPWMPGTPLRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWVYGFVRACLRLVPE
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWVYGFVRACLRLVPE
QY 481 RHNERRFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHF
Db 481 RHNERRFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHF
QY 541 LAKFLHWMMSVYVVELLRSFFVYTTTTFQKNRLLFFYRKSVWSKLSIGIRQHLKE
Db 541 LAKFLHWMMSVYVVELLRSFFVYTTTTFQKNRLLFFYRKSVWSKLSIGIRQHLKE

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lication US/09402181B

839

WATION:

I: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
SEQUENCES: 633
SEQUENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
SET: Two Embarcadero Center, Eighth Floor
y: San Francisco
IE: California
NTRY: USA

: 94111-3834
READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
WARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
LICATION NUMBER: US/09/402,181B
ING DATE: 29-Sep-1997
SSIFICATION: <Unknown>
PLICATION DATA:
LICATION NUMBER: US 08/724,643
ING DATE: 01-OCT-1996
LICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
ICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
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Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCI
Db |||||
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCI
Db |||||
QY 61 DARPPPAAPSFQVSLKELVARVLQRLCERGAKNVLAFFGALLDGGAGGPPPEAF
Db |||||
QY 61 DARPPPAAPSFQVSLKELVARVLQRLCERGAKNVLAFFGALLDGGAGGPPPEAF
Db |||||
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPL
Db |||||
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPL
Db |||||
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLP
Db |||||
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLP
Db |||||
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Db |||||
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Db |||||
QY 541 LAKFLHLMMSVYVVELLRSSFFVYVTTTTFQKNRLLFFYRKSWSKLSQSIGIRQLKR
Db |||||

EAHVQRHREARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
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plication US/09721456
7110
RMATION:
NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
SEQUENCES: 727
NDENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
RY: San Francisco
ATE: California
NTRY: USA
P: 94111-3834
3 READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
FTWARE: Patent in Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/09721,456
LING DATE: 22-No. 6617110-2000
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: US/08/974,549A
LING DATE: 19-NOV-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
PLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-721-456-2
Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLPGQWRLVQRGDPAAFRALVAQC
Db 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLPGQWRLVQRGDPAAFRALVAQC
QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEEA
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEEA
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPP
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPP
QY 181 ATOARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSPL
Db 181 ATOARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSPL
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Db 301 ROHHAGPSTSRPPRPWDTPCPPVYAETKHFYSSGDKQLRPSFLLSSLRPSL
QY 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPI
Db 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPI
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Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPWQVYGFVACLRRLVPI
QY 481 RHNERRFLRNTKFKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHI
Db 481 RHNERRFLRNTKFKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHI

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CFLHLMSSVVVVELLRSEFFVYVTTTFQKNRLLFFYKRSVWSKLSIGIRQHLKRVQLRE 600
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SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVQCQIPQGSILSTL 840
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RHRVTYVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSPDFXTILD 1132
RHRVTYVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSPDFXTILD 1132

Publication US/09953052

619
MATION:
T: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
OF SEQUENCES: 72
NDENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
EET: Two Embarcadero Center, Eighth Floor
Y: San Francisco
TE: California
NTRY: USA
: 94111-3834
: READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
WARE: Patent in Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/09/953,052
ING DATE: 14-Sep-2001
SSIFICATION: <Unknown>
PLICATION DATA:

APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
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APPLICATION NUMBER: US 08/911,312
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPQGWRLVQVGPAAAFRALVAQCI
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPQGWRLVQVGPAAAFRALVAQCI
Qy 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAI
Db 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAI
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Db 121 SYLNTVTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
Qy 181 ATQARPPPHASGPRRRRLGCERAWNSHVRVREAGVPLGLPAPGARRRGGASRSPLPI
Db 181 ATQARPPPHASGPRRRRLGCERAWNSHVRVREAGVPLGLPAPGARRRGGASRSPLPI
Qy 241 GAPEPERTPVQGSWAHPGTRGSDRGFCVVSPARPABEATSLEGALSGRHE
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Qy 301 RQHAGPPSTSRPPRPWDTPCPVPVYAEKHFYSSGDKQLRPSFLLSSLRPSLT
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RLTEVIAIIPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780
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SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQGSILSTL 840
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RHRVTYVPLGLSLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132
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1
Application US/08974549A
178

ATION:

Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
ENTION: Human Telomerase Catalytic Subunit
QUENCES: 727
ICE ADDRESS:
Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San Francisco
California
USA
1-3834

ABLE FORM:

E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154
OTHER INFORMATION: /note= "fusion protein composed of hTERT
protein sequence, vector sequences, the
OTHER INFORMATION: Myc epitope and His6 tag"
US-08-974-549A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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Db 61 DARPPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPPEAF
Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
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| 1RHRVTVVPLLGSLRTAQTQLSRKLPGTTLTALAAAAANPALPSDFKTILD | 1132 |
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```

/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGN
/ TITLE OF INVENTION: THERAPEUTIC METHODS
/ NUMBER OF SEQUENCES: 335
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/912,951
/ FILING DATE: 14-AUG-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002600US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 323:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1154 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-912-951-323

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application US/08912951

789

ATION:

HILLON.
Cecilia Thomas D.

LECII, THOMAS R.
Linnæus Teaching-

Lingner, Joachm
Nakamura, Toru

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11 application US/09402181B
0839
MATION:
JT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154
OTHER INFORMATION: /note= "fusion protein composed of
protein sequence, vector sequences, the
Myc epitope and His6 tag"
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US-09-402-181B-611

Query Match 100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
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RESULT 15
US-09-721-456-611
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; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; OTHER INFORMATION: /note= "fusion protein composed of
; protein sequence, vector sequences, the

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: epitope and His6 tag"
: DESCRIPTION: SEQ ID NO: 611:
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)
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Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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| 00.0 | 1132 | 9 | US-09-749-728B-31 | Sequence 31, Appl |
| 00.0 | 1132 | 9 | US-09-843-676-225 | Sequence 225, App |
| 00.0 | 1132 | 9 | US-09-953-052-2 | Sequence 2, Appli |
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| 00.0 | 1132 | 12 | US-10-388-578-2 | Sequence 2, Appli |
| 00.0 | 1132 | 14 | US-10-053-758-225 | Sequence 225, App |
| 00.0 | 1132 | 14 | US-10-208-243-2 | Sequence 2, Appli |
| 00.0 | 1132 | 14 | US-10-054-295-225 | Sequence 225, App |
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| 00.0 | 1132 | 14 | US-10-044-692-2 | Sequence 2, Appli |
| 00.0 | 1132 | 14 | US-10-044-539-2 | Sequence 2, Appli |
| 00.0 | 1132 | 14 | US-10-295-681-57 | Sequence 57, Appl |
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| 45 | 2184 | 36.6 | 438 | 14 | US-10-294-778-10 | Sequenc |

ALIGNMENTS

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; Sequence 2, Application US/099900080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258c
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-080-2

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| Best Local Similarity | 100.0% | Pred. No. 0; | | |
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Application US/09749728B
020142457A1
TION:
zawa, Akihiro
ta, Jun-Ichi
kuda, Keiichi
awa, Satoshi

|||APPLICANT: Sakurada, Kazuhiro
|||APPLICANT: Gojo, Satoshi
|||APPLICANT: Yamada, Yoji
|||TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENT
|||FILE REFERENCE: 00766.00043
|||CURRENT APPLICATION NUMBER: US/09/749,728B
|||CURRENT FILING DATE: 2001-09-17
|||PRIOR APPLICATION NUMBER: H11-372826
|||PRIOR FILING DATE: 1999-12-28
|||PRIOR APPLICATION NUMBER: PCT-JP00-01148
|||PRIOR FILING DATE: 2000-02-28
|||PRIOR APPLICATION NUMBER: PCT-JP00-07741
|||PRIOR FILING DATE: 2000-11-02
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|||US-09-749-728B-31

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IT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
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OF SEQUENCES: 225
NDENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
CY: San Francisco
TE: California
NTRY: United States of America
Y: 94111
READABLE FORM:
PUTER TYPE: Floppy disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
WARE: PatentIn Release #1.0, Version #1.30
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ING DATE: 26-Apr-2001
SSIFICATION: 536
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ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
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ING DATE: 01-OCT-1996
AGENT INFORMATION:
E: Apple, Randolph T.
ISTRATION NUMBER: 36,429
ERENCE/DOCKET NUMBER: 015389-002930US
UNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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TYPE: amino acid
TOPOLOGY: linear
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US-09-843-676-225
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Best Local Similarity 100.0%; Pred. No. 0;
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RMATION:
NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
F INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
OF SEQUENCES: 72
NDENCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
TY: San Francisco
ATE: California
JNTRY: USA
P: 94111-3834
R READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/09/953,052
ING DATE: 14-Sep-2001
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: 09/052,919
ING DATE: <Unknown>
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/854,050
ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/911,312
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/912,951
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/915,503
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/974,549
ING DATE: 19-NOV-1997
PLICATION NUMBER: US 08/974,584
ING DATE: 19-NOV-1997
PLICATION NUMBER: WO PCT/US97/17618
ING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2
Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQGDPAAFRALVAQC
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQGDPAAFRALVAQC
QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGGGPPPEA
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGGGPPPEA
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
QY 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGGASRSRLPL
Db 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGGASRSRLPL
QY 241 GAAPERTPVGQSWAHGPRTRGPSDRGFCVSPARPAEEATSLGALSGRH
Db 241 GAAPERTPVGQSWAHGPRTRGPSDRGFCVSPARPAEEATSLGALSGRH
QY 301 ROHHAGPPSTSRPPRPWDTPCPPVYAEKHFYSSGDKQLRPSFLSSLRPSL
Db 301 ROHHAGPPSTSRPPRPWDTPCPPVYAEKHFYSSGDKQLRPSFLSSLRPSL
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLLVP
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLLVP
QY 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEH
Db 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEH
QY 541 LAKFLHMLMSVYVVELLRSFFVYTTTFQKNRLLFFYKRSVWSKLQSIGIRQHLK
Db 541 LAKFLHMLMSVYVVELLRSFFVYTTTFQKNRLLFFYKRSVWSKLQSIGIRQHLK
QY 601 LSEAEVROHREARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERL
Db 601 LSEAEVROHREARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERL
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTC
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTC
QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMR
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMR

11:43:37 2004

us-09-424-686f-2.rapb

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| TSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL | 840 |
| 3LCYGD MENKLFAGIRRDG LLLRLVDDFLLVTPH LTHAKTFLRTLVRGVPEYGCVVNL | 900 |
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| TVVNFPPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF | 960 |
| TVVNFPPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF | 960 |
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| 3FKAGRNMRRKLFGLVRLKXCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP | 1020 |
| QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL | 1080 |
| QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL | 1080 |
| PRHRVTYVPLLGSLRTAQTOISRKLPGTTTLTALEAAANPALPSDFKTILD | 1132 |
| PRHRVTYVPLLGSLRTAQTOISRKLPGTTTLTALEAAANPALPSDFKTILD | 1132 |

publication US/10388578
; US20030224411A1

ATION:
 ron Corporation
 tantan, Lawrence
 alph, Brandenberger
 oseph, Gold D.
 ohn, Irving
 andalam, Ramkumar
 ok, Michael
 helton, Dawne
 NTION: Genes that are Up- or
 NTION: Embryonic Stem Cells
 E: 135/001
 CATION NUMBER: US/10/388,578
 G DATE: 2003-03-13
 ID NOS: 139
 tom

no sapiens

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100.0%; Score 5961; DB 12; Length 1132;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RPPAAPSPFQVSCIKELVARVLQRLCERGAKNVLAFCFALLDGAAGGPPDEAFTTSVR 120
 |||||
 RPPAAPSPFQVSCIKELVARVLQRLCERGAKNVLAFCFALLDGAAGGPPDEAFTTSVR 120
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LPNTVTDALRGSGAWGLILRRVGDVTLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

'QARPPPHASGPRRLGGERAWNHSVREAGVPLGUPAGARRGGGSASRSUPLPKRPRR 240

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|--|
| QY | 241 | GA | PE | P | T | P | V | G | Q | S | W | A | H | P | G | R | T | R | G | P | S | D | R | G | F | C | V | V | S | P | A | R | P | A | E | A | T | S | L | E | G | A | L | S | G | T | R | H | |
| Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 301 | RQ | H | A | G | P | P | S | T | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-10-053-758-225
; Sequence 225, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
;

Andrews, William H.
INVENTION: No. US20030032075A1el Telomerase
SEQUENCES: 225
SEQUENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
LET: Two Embarcadero Center, 8th Floor
Y: San Francisco
TE: California
NTRY: United States of America
P: 94111
READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
TWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/053,758
ING DATE: 18-Jan-2002
SSIFICATION: 536
PLICATION DATA:
PLICATION NUMBER: US/08/854,050
ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
ING DATE: 01-OCT-1996
AGENT INFORMATION:
E: Apple, Randolph T.
ISTRATION NUMBER: 36,429
ERENCE/DOCKET NUMBER: 015389-002930US
UNICATION INFORMATION:
EPHONE: (415) 576-0200
EFAX: (415) 576-0300
OR SEQ ID NO: 225:
CHARACTERISTICS:
GTH: 1132 amino acids
E: amino acid
OLOGY: linear
TYPE: protein
DESCRIPTION: SEQ ID NO: 225:

100.0%; Score 5961; DB 14; Length 1132;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 361 VETIFLGSRPWMPGTERRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP
Db 361 VETIFLGSRPWMPGTERRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP
QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPQVYGFVRACLRLVLP
Db 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPQVYGFVRACLRLVLP
QY 481 RHNERFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCVPAAEH
Db 481 RHNERFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCVPAAEH
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Db 541 LAKFLHMLMSVYVVELLRSEFFVYVTTTFQKNRLLFFYRKSVWSKLQSIGIRQHLK
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFREKRAERL
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFREKRAERL
QY 661 LFSVLNBERARRPGLLGASVLGDDIHRAWRTFVLRVRAQDPPPELYFVKVDVT
Db 661 LFSVLNBERARRPGLLGASVLGDDIHRAWRTFVLRVRAQDPPPELYFVKVDVT
QY 721 PODRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMR
Db 721 PODRLTEVIASIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMR
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Db 781 QETSPLRDAVVIEQSSSLNEASSGLFDFLRFMCHHAVRIRGKSVYQCGIPIQG
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Db 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRLVRGVPEY
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Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDYSSYARTSI
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Db 961 NRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA
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Db 1021 FHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAAGAGPLPSEAVQWLC
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Db 1081 KLTRHRVTYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDEKTLTD 1

RESULT 8
US-10-208-243-2
Sequence 2, Application US/10208243
Publication No. US2003004394A1
GENERAL INFORMATION:
APPLICANT: Gaeta, Federico C.A.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Imm
TITLE OF INVENTION: Response to a Telomerase Antigen
FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: US/10/208,243
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/675,321
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2

entln Ver. 2.0

no sapiens

100.0%; Score 5961; DB 14; Length 1132;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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NERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
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EAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
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SLCYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRLVGVPEYGCVVNL 900
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TTVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLT 960

Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSI
QY 961 NRGEKAGRNMRRLKFLGVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHA
Db 961 NRGEKAGRNMRRLKFLGVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHA
QY 1021 FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC
Db 1021 FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC
QY 1081 KLTRHRVTYVPLGLSLRTAQTLRSKRLPGTTLTALEAAANPALPSDFKTILD 1
Db 1081 KLTRHRVTYVPLGLSLRTAQTLRSKRLPGTTLTALEAAANPALPSDFKTILD 1

RESULT 9

US-10-054-295-225
; Sequence 225, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-295-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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|AGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRLVPPGLWGS 480
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|
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|KFLHWMMSVYVVELLRSFFYVTTETTFQKNRLFYRKSVWSKLQSIGIRQHLKRVQLRE 600
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|SVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
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|DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
|
|DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
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|TSPLRDAVVEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCGIPIQGSILSTL 840
|
|TSPLRDAVVEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCGIPIQGSILSTL 840
|
|SLCYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRLVRGVPYGCVVNL 900
|
|SLCYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRLVRGVPYGCVVNL 900
|
|TVNVFVVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
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|TVNVFVVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
|
|GFKAGRNMRRKLFGLVRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
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application US/10105963
> US20030068818A1
*ATION:

; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Com
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determina
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-963-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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Db 121 SYLENTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPI
Qy 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASASRLPI
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Db 481 RHNERRFLRNTKKFISLKGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEI
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Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVI
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RRHRTYVPLLSGLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
plication US/10044692
US20030096344A1
MATION:
T: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
OF SEQUENCES: 335
NDENCE ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
Y: San Francisco
ATE: California
NTRY: United States of America
P: 94111
READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
WARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/044,692
ING DATE: 11-Jan-2002
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: 08/912,951
ING DATE: <Unknown>
PLICATION NUMBER: US 08/854,050
ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
ING DATE: 01-OCT-1996
Y/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2
Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQC
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQC
QY 61 DARPPPAAPSPRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEEA
Db 61 DARPPPAAPSPRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEEA
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPP
QY 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSSASRLPL
Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSSASRLPL
QY 241 GAAPEPERTVCGQSWAHGPRTRGSPDRGFCVVSAPPAEATSLGALSGRH
Db 241 GAAPEPERTVCGQSWAHGPRTRGSPDRGFCVVSAPPAEATSLGALSGRH
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Db 301 ROHHAGPPSTSRPPRPWDTPCPPVYAEKHFYSSGDKQLRPSFLLSSLRPSL
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Db 361 VETIFLGSRPWMPGTPLRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP
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Db 421 PAAGVCAREKPOGSVAAPAEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVP
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QY 541 LAKFLHMLMSVVVVELLSRFFVYVTTTTPQKNLFFYRKSVWSKLSQIGIRQHLK
Db 541 LAKFLHMLMSVVVVELLSRFFVYVTTTTPQKNLFFYRKSVWSKLSQIGIRQHLK
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKKAERL
Db 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKKAERL
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVT
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVT
QY 721 PQDRLTEVIAIIPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTLDQPYMR
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QY 781 QETSPLRDAVVEIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQGS
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plication US/10044539
US20030100093A1
RMATION:
NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
F INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
OF SEQUENCES: 335
ONDNCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
TY: San Francisco
ATE: California
UNTRY: United States of America
P: 94111
R READABLE FORM:
DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/044,539
LING DATE: 11-Jan-2002
ASSIFICATION: 435
PLICATION DATA:
PLICATION NUMBER: 08/912,951
LING DATE: <Unknown>
PLICATION NUMBER: US 08/854,050
LING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/851,843
LING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
GISTRATION NUMBER: 36,429
FERENCE/DOCKET NUMBER: 015389-002600US
MUNICATION INFORMATION:
LEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-539-2
Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQC
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQC
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Db 61 DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGARGGPPPEA
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Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY

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plication US/10295681
US20030166270A1
TION:
Premkumar Reddy
shil G. Rane
chard V. Mettus
TION: COMPOSITIONS AND METHODS FOR REVERSIBLY
TION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS
: 6056-307
ATION NUMBER: US/10/295,681
: DATE: 2002-11-15
ION NUMBER: US 60/334,760
ATE: 2001-11-15
ID NOS: 69
SEQ for Windows Version 4.0
o sapiens
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVT
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVT
QY 721 PQDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLQPYMR
Db 721 PQDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLQPYMR
QY 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOG
Db 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOG
QY 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY
QY 901 RKTVVNFPEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSII
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QY 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA
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QY 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWL
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QY 1081 KLTRHRTVTVPLIGSLRTAQTLRSKRLPGTTLTALEAAANPALPSDFKTILD 1
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RESULT 15
US-10-325-810-611
; Sequence 611, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

SRATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:

PLICATION NUMBER: US/10/325,810
LING DATE: 20-Dec-2002

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: US/09/402,181

LING DATE: 29-Sep-1997

PLICATION NUMBER: US 08/724,643

LING DATE: 01-OCT-1996

PLICATION NUMBER: US 08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US 08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US 08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/911,312

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/912,951

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/915,503

LING DATE: 14-AUG-1997

PLICATION NUMBER: WO PCT/US97/17885

LING DATE: 01-OCT-1997

AGENT INFORMATION:

AE: Ausenhus, Scott L.

ISTRATION NUMBER: 42,271

ERENCE/DOCKET NUMBER: 015389-002620US

UNICATION INFORMATION:

EPHONE: (415) 576-0200

EFAX: (415) 576-0300

OR SEQ ID NO: 611:

3 CHARACTERISTICS:

NGTH: 1154 amino acids

DE: amino acid

RANDEDNESS: <Unknown>

POLOGY: linear

E TYPE: protein

AE/KEY: Protein

ATION: 1.1154

ER INFORMATION: /note= "fusion protein composed of hTERT

rotein sequence, vector sequences, the

epitope and His6 tag"

DESCRIPTION: SEQ ID NO: 611:

L

ilarity 100.0%; Score 5961; DB 12; Length 1154;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
APRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60

APPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
APPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

APNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
APNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

APPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
APPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

APPERTPVQGSWAHPGTRTGRGSDRGFCVVSPPARPAEEATSLGALSGTRHSHPSVG 300
APPERTPVQGSWAHPGTRTGRGSDRGFCVVSPPARPAEEATSLGALSGTRHSHPSVG 300

QY 301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSL
Db 301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSL
QY 361 VETIFLGSRPWMPGTPRRRLPRLPQRYWQMEPLFLELLGNHAQCPYGVLLKTHCP
Db 361 VETIFLGSRPWMPGTPRRRLPRLPQRYWQMEPLFLELLGNHAQCPYGVLLKTHCP
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRLVLP
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRLVLP
QY 481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEH
Db 481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEH
QY 541 LAKFLHMLMSVYVVELLRSFFVYTTTFFQXNRLFFYRKSVWSKLQSIGIRQHLK
Db 541 LAKFLHMLMSVYVVELLRSFFVYTTTFFQXNRLFFYRKSVWSKLQSIGIRQHLK
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERL
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERL
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVT
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVT
QY 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMR
Db 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMR
QY 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOG
Db 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOG
QY 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY
Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY
QY 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSI
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSI
QY 961 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA
Db 961 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA
QY 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCI
Db 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCI
QY 1081 KLTRHRVTYVPLLGSRLTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1:
Db 1081 KLTRHRVTYVPLLGSRLTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1:

Search completed: April 22, 2004, 00:23:55
Job time : 359 secs

GenCore version 5.1.6
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tein search, using sw model

April 21, 2004, 23:46:16 ; Search time 30 Seconds
(without alignments)
3629.627 Million cell updates/sec

US-09-424-686F-2

5961

1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTILD 1132

BLOSUM62

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

hits satisfying chosen parameters: 283366

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_78:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

| Query | Match | Length | DB | ID | Description |
|-------|-------|--------|--------|----|--------------------|
| 100.0 | 1132 | 2 | T03844 | | telomerase catalyt |
| 12.2 | 1123 | 2 | T51517 | | telomerase reverse |
| 10.0 | 989 | 2 | T03838 | | telomerase catalyt |
| 6.6 | 1132 | 2 | T31107 | | telomerase reverse |
| 6.1 | 1117 | 2 | T14891 | | telomerase (EC 2.7 |
| 6.0 | 884 | 2 | S53396 | | telomerase catalyt |
| 3.0 | 3530 | 2 | A59266 | | unconventional myo |
| 2.9 | 660 | 1 | QQBE3 | | BHLF1 protein - hu |
| 2.4 | 3511 | 2 | A59295 | | unconventional myo |
| 2.4 | 1560 | 2 | T00080 | | hypothetical prote |
| 2.4 | 1892 | 2 | T18314 | | hypothetical prote |
| 2.3 | 1460 | 1 | EDBEIF | | immediate-early pr |
| 2.3 | 552 | 2 | F75311 | | ABC transporter, A |
| 2.3 | 924 | 2 | S27923 | | gene LF3 protein - |
| 2.3 | 1356 | 1 | C45219 | | N-methyl-D-asparta |
| 2.3 | 946 | 2 | JC7810 | | inositol 1,4,5-tri |
| 2.2 | 606 | 2 | G75302 | | orotidine 5'-phosp |
| 2.2 | 1106 | 2 | JQ0405 | | hypothetical 119.5 |
| 2.2 | 860 | 2 | S55543 | | RNA-directed DNA p |
| 2.2 | 1184 | 2 | G01763 | | atrophin-1 - human |
| 2.2 | 1446 | 1 | A45344 | | immediate-early pr |
| 2.2 | 1184 | 2 | S50832 | | atrophin-1 - human |
| 2.2 | 2715 | 2 | T13049 | | eyelid - fruit fly |
| 2.2 | 383 | 2 | S32975 | | gene BCRF2 protein |
| 2.2 | 403 | 2 | S52796 | | prpL2 protein - hu |
| 2.2 | 1776 | 2 | G86280 | | protein T5E21.13 [|
| 2.2 | 628 | 2 | S01955 | | hypothetical prote |
| 2.1 | 376 | 2 | C75580 | | adenine deaminase- |
| 2.1 | 1048 | 2 | T31425 | | C-terminal domain- |

| | | | | | | |
|----|-------|-----|------|---|--------|-----------|
| 30 | 127 | 2.1 | 260 | 2 | S22373 | proline- |
| 31 | 127 | 2.1 | 505 | 2 | S72273 | actin-dej |
| 32 | 127 | 2.1 | 580 | 2 | T43481 | probable |
| 33 | 127 | 2.1 | 847 | 1 | A53800 | mixed-li |
| 34 | 127 | 2.1 | 862 | 2 | T46289 | hypothet |
| 35 | 127 | 2.1 | 1039 | 2 | T35878 | hypothet |
| 36 | 126.5 | 2.1 | 603 | 2 | H75272 | probable |
| 37 | 126 | 2.1 | 330 | 2 | E98119 | transpos |
| 38 | 126 | 2.1 | 1067 | 2 | T18196 | pol prot |
| 39 | 125.5 | 2.1 | 574 | 2 | T43556 | Wiskott- |
| 40 | 125.5 | 2.1 | 574 | 2 | T38819 | wiskott- |
| 41 | 125 | 2.1 | 522 | 2 | S52216 | viral pr |
| 42 | 125 | 2.1 | 1914 | 2 | T42635 | tenascin |
| 43 | 124 | 2.1 | 1298 | 1 | EDB75 | immediat |
| 44 | 124 | 2.1 | 1323 | 2 | S27224 | N-methyl |
| 45 | 123.5 | 2.1 | 381 | 2 | S16506 | hypothet |

ALIGNMENTS

RESULT 1
T03844
telomerase catalytic chain - human
N;Alternate names: telomerase reverse transcriptase
C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-
C;Accession: T03844
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrew
Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast ar
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03844
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1132 <NAK>
A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PJ
A;Experimental source: kidney
C;Genetics:
A;Gene: TRT
A;Map position: 5p

| | | | | |
|-----------------------|-----------------|---------------------------------|-----------------------------------|--------------|
| Query Match | 100.0%; | Score 5961; | DB 2; | Length 1132; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1132; | Conservative 0; | Mismatches 0; | Indels 0; | |
| QY | 1 | MPRAPRCRAVRSLLRSHYREVLP | PLATFVRRRLGPGQWRLVQRGDPAAFRALVAQC | |
| Db | 1 | MPRAPRCRAVRSLLRSHYREVLP | PLATFVRRRLGPGQWRLVQRGDPAAFRALVAQC | |
| QY | 61 | DARPPPAAPSFQVSCLELVARVLQRLCERGA | KNVLAFGFALLDGARGGPEF | |
| Db | 61 | DARPPPAAPSFQVSCLELVARVLQRLCERGA | KNVLAFGFALLDGARGGPEF | |
| QY | 121 | SYLPNTVTDALRGSGAWGLLLRRVGGDDVL | VHLLARCALFVLVAPSCAYQVCGPE | |
| Db | 121 | SYLPNTVTDALRGSGAWGLLLRRVGGDDVL | VHLLARCALFVLVAPSCAYQVCGPE | |
| QY | 181 | ATQARPPPHASGPRRLGGERAWNHVSREAG | VPLGLPAPGARRRGGASRSPLI | |
| Db | 181 | ATQARPPPHASGPRRLGGERAWNHVSREAG | VPLGLPAPGARRRGGASRSPLI | |
| QY | 241 | GAAPPEPRTPVGQGSWAHPGRTGRGSDRG | FCVVSPPARPAEATSLEGALSGRH | |
| Db | 241 | GAAPPEPRTPVGQGSWAHPGRTGRGSDRG | FCVVSPPARPAEATSLEGALSGRH | |
| QY | 301 | RQHHAGPPSTSRPPRPWDTPCPPVYAE | TKHFLYSSGDKQLRPSFLLSLRPSL | |
| Db | 301 | RQHHAGPPSTSRPPRPWDTPCPPVYAE | TKHFLYSSGDKQLRPSFLLSLRPSL | |
| QY | 361 | VETIFLGSRPWMPGTPRRRLPRLPQRY | WQMRPLFLELLGNHAQCPYGVLLKTHCP | |
| Db | 361 | VETIFLGSRPWMPGTPRRRLPRLPQRY | WQMRPLFLELLGNHAQCPYGVLLKTHCP | |

AGVCAREKPOGSAAPAEEDTDPRRLVOLLRHQSSPQWVYGFVACLRRLVPPGLWGS 480
|||||
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INERRFLRNTKPFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
|||||
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SVLNVERARRPGLLGASVGLGLDDIHRAWRTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
|||||
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DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
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TSPLRDVAVVIEQSSSLNEASSGLFDFVFLRFMCHHAVRIRKSVYQCQGIPOGSI LSTL 840
|||||
TSPLRDVAVVIEQSSSLNEASSGLFDFVFLRFMCHHAVRIRKSVYQCQGIPOGSI LSTL 840
SLCYGDMENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
|||||
SLCYGDMENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
TVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
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TRHRTVYVPLLGSLRTAQTLQSRKLP GTTTLTALEAANPALPSDFKTILD 1132
TRHRTVYVPLLGSLRTAQTLQSRKLP GTTTLTALEAANPALPSDFKTILD 1132

se transcriptase - Arabidopsis thaliana
s: protein F5E19 190
dopsis thaliana (mouse-ear cress)
000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
517
mura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New
Protein Sequence Database, August 2000
er: 225394
517
inary
DNA
23 <SAT>
es: EMBL:AL391147
ource: cultivar Columbia; BAC clone F5E19

5
; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
0

ilarity 12.2%; Score 724.5; DB 2; Length 1123;
23.8%; Pred. No. 1e-41;

Matches 294; Conservative 199; Mismatches 511; Indels 233;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFV-----RRLGPOGWR-----
Db |||||
1 MPRKPRHRVPEILWRLFGNARNLNDIVLIPNRNIQEQCRGCGGCLGCS
QY 39 VQGDPAAFRALVAQCLVCPWDARPPPAAPSFQVSCIKELVARVLQRL---
Db |||||
61 LRSDDPIHYRKLHRCFV-VLHEQTPLLDPSPTSWNSQREIVERIEMMQSGC
QY 96 VLAQGFALLDGARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDV
Db |||||
118 VICARYDKYDQS-----SPILELT-SSSWEFLLRVGHV
QY 156 CALFVLVAPSCAYQVCGPPPLYQLGAAT-----QARPPPHASGPRRRRLGCERAW
Db |||||
160 TSIFLPLLGKHQVSGPPPLCIKHKRTLSVHENKRRKDDNVQPPTKRQWLSSA
QY 210 AGVPLGLPAPG---ARRRGSASRSLPLKPRRGA-----APEPERTP
Db |||||
220 DSATI-TPIVGEDVDQHREKKTTRSRILYLRKRRKQKYNFKKVDNAPCITP
QY 258 HPGRTGPSDRGFCVVSAPPAEAEATSLGALSGTRHSHPSVGRQHAGPPST
Db |||||
272 ---STNGKVSTG-----NDEMNLHIGINGSLTDFVKQAKQ-----
QY 318 DTPCPPVYAETKHELYS-SCDKBQLRPSFLLSLRSLTGARRLVETIFLGSRE
Db |||||
304 -----VKRNKNFKFGLSEYTVIPPNHILKTLRENCSDSKLLMNHIFGEVNT
QY 377 RRLPRLPQ---RYWQMRPLFLELLGNHQAQCPYGVLLKTHCP-----LRAP
Db |||||
357 HKGNCPSGSICLYHSLKSLKNLIGTKSSHLKMLLDKHCPCVLLQLQEDALKSG
QY 425 VCAREK-----POGSVAA---PEEDTDPRRLVOLLRHQSSPQWVYGFVACLR
Db |||||
417 --RRQADKLPHGSSSQTGKPCPSVEERKL-----YCTNDQVVSFIWAICR
QY 477 LWGSRHNERFLRNTKPFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVF
Db |||||
469 LLGTHQMRVLRKNIAMFVSRRRNEKCTVNOFLHKVKSDFPFFARKE--LCCV
QY 537 REE-----ILAKELHLMMSVYVVELLRSFFVVTETTFQKNRLFFYRKSVWS
Db |||||
527 QSESIRSTQOMLCTKWISWLFLEIVKLVHFNFFATESQGRNLIIYYRKRSE
QY 589 IRQHLKRVQLRELSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVG
Db |||||
587 ISKALDGYVLVDDAEASSRKK-----LSKFRPLPKANGVRMVL-----
QY 649 KRAERLTSRVKALFESVLNVERARRPGLLGASVGLGLDDIHRAWRTFVLVRQAQDP
Db |||||
631 SRSQSL-----RDTHAVLKDIOQLKEPDVLGSSVDFDHDFFYRNLCPLYLIHLRSQSG
QY 708 FVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGH-----V
Db |||||
687 FVADVFKAFDSVDQGLLHVIOQFLKDE--YILNRCLVCCGKRSNWVNKILV
QY 762 HVSTLTDLPYMRQFVAHLQETSPLRDVAVVIEQSSSLNEASSGLFDFVFLRFMCH
Db |||||
745 NPSRFTSTVPYNA-----LQ-----SIVVDKGENHRVRKDLVVMWIGNMLKN
QY 822 GKSIVQCGIQSGSILSTLLCSLCYGDMMENKLPAGI-----RRDG
Db |||||
793 KSFYVQIAGIPQGHRLSSLLCCFYGYGHLETLIYFFLEASKDVSSKECSREEE
QY 863 --LLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNLKRTVVNFPVEDE--
Db |||||
853 YKLLRFIDDLVLFVSTSRDQASSFTHRLKHGFKDYNCFMNETKFCINFEDKKEHR
QY 913 --ALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTFNRGF
Db |||||
913 FVGDNVGVFVR-----WTGLLINSRTFEVQVDYTRYLSGHISSTFSVAWQN

[illegible]

6.6%; Score 395; DB 2; Length 1132;
ilarity 22.2%; Pred. No. 5.9e-19;
Conservative 114; Mismatches 305; Indels 58; Gaps 15;
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FEYQDQRIQISNLTETEFVANVPKFNLEGK-NKKIFNKKMLQFVKFNRFSFTKISLL 509
MSVRDCAWLRRSPGVCVPAAEH---RLREELAKFLHMLMSVYVVELLRSPFYVTE 566
FRVNEVSWL---SFCKDENKKFFMNEHVFVKLKWFFEDLAITLMRCVYFSTK 565
QKRLFFYKSVWSKLQSIGIRQHKLKRVQLRELSEAEVRQHRARPALLTSRLRFIPK 626
EYQIRFYKKNIMMRLSIDDLLKQ-NLKQVEKEMRIFCESQ-NFAPGKRLIPK 623
ELRPIVMDYVVGARTFRRE---KRAERLTSRVK---ALFVSLNVERARRPGLLG 677
CFRPIM---TFNRKIPNOVGKFKQSRMTNNKLTQTAHMLKLNKSKMFKHSFG 674
ZLGDDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAS----- 731
JFNYDDIMKRYENFVQKWK-QINSPKLYFVAMDIEKCYDNVDCEVNVNFKLSQSDLM 733
-----IIPQNTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLQVNRQFVAHLQET 783
PILNTFVLKRNINVERSNFRKLPKIKQFYRYKPKQ-IGIDGSSYPTLFEILEDEFND 792
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KRTIIVEQEQRKKFPKNDLQPVLKICQNNYVTFNKKQYKQKMGIPQGLCVSYILSS 852
GDMENKLFAGIRRD-----GLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPY 894
ANLEENALQFLRKESMDPEKPEINLLMLRLTDDYLLMTTEKNAMLFIEKLYQLSLGN 912
VNLRKTNNVFPVEDEALGTAFAVQ---MPAHGLFPWCGLLLDTRILEVQSDYSSYAR 951
CFMKKLTNFALNLQKIGCTNTTQDIDSINDDLFWHIGISIDIKLNIQNI-NIKK 971
RASLTFNRGEKAGNRMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYR 1011
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CVLQLP-FHQ 1023
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7.7.-) catalytic chain p133 - Tetrahymena thermophila
telomerase reverse transcriptase
ymena thermophila
99 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
ndhi, L.
Sci. U.S.A. 95, 8485-8490, 1998
rse transcriptase component of the Tetrahymena telomerase ribonucleopro
x: Z18252; MUID:98337941; PMID:9671704
91
nary; translated from GB/EMBL/DDBJ
mRNA
7 <COL>
s: EMBL:AF061284; NID:g3335166; PID:g3335167; PIDN:AAC39140.1

GC5
otidyltransferase
6.1%; Score 363; DB 2; Length 1117;
larity 20.2%; Pred. No. 9.3e-17;
Conservative 160; Mismatches 368; Indels 234; Gaps 35;

QY 322 PPVYAEKHLVSSGDKQLRPSFLLSSLRPSLTGARRLVETIFLGRSPWMPGT
Db 239 PGVF-KSSFFNYS-----EIKKGQFQKVIQEKLGQRQ-----FINSDKIKPDH
QY 382 --LPQRY-----WQMRPLFLE---LLGNHAQCPYGVLLKTHCPLRAAVTPA
Db 287 KTLKEYQSKNPSQCEERDLFLETEKIVQFNHNFNINFNLLKKFKCL-----
QY 429 EKPGSVAAPBEEDTPRRLVQLLRQS-----SPWQVYG
Db 334 -----PENYQSLKSQVKQIVQSENKANQOSCENTLSLYDTISYKQITN
QY 470 RRLVPPGLWGRSRHNRERFLRNTKKFISLGKHAKLSQLTWMKSVRDCAWLRRS
Db 385 QNCVPNQLLGKK-NFKVFLEKLYEFVQMKRFENQKVDLYICFMDVDFVEWF---
QY 530 PAAEHLR-----REEILAKFLHMLMSVYVVELLRSEFFYVTTTFQKNRLF
Db 436 DLKNQKFTQKRKYISDKRKILGDLIVFIINKIVIPVLRYNFYITEKHKEGSGQIF
QY 581 W---SKQSIGI-RQHLKRVQLRELSEAEVRQHRARPALLTSRLRFIPKPDGL
Db 496 WKLVSCLTIVKLEENLEKVEEKLIPEDSFQKYPQ-----GKLRIPKKGSGF
QY 637 DYVGARTFRREKRAERLTSRVKALFS-----VLNYERARRPGLLGASVGLDDDI
Db 547 -----TFLRKDKQKNIKLNQILMDSQLVFRNLKMLGQKIGYSVFDNKKQI
QY 693 FVLVRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKQNTYCVRRYAV
Db 600 FIEKWKNG-RPQLYYVTLDIKKCYDSIDQMKLLNFFNQSDLIQDTYFINKYLL
QY 753 GHVRKAFKSHVSTLTDLQ-----PYM-----RQFVAHLQE---
Db 659 PLLQIQOTNNLNSAMEIEEEKINKKPFKMDNINFPYYFNKLERQIAYSLYDDDD
QY 783 ---TSLRDVAVIEQSSILNEASSGLFDVFLRFMCHHVRIRGKSYVQCQIGIP
Db 719 FKEIQSDDRPPIVINQDKPRCITKDIHNLHKLHISQNVISFNKVKFRQKRGIP
QY 839 TLLCSLCYGDMMENKLFAGIRRD-----GLLLRLVDDFLLVTPHLLTHAKTFLR
Db 779 GVLCSFYFGKLEEEYTQFLKNAEQVNGSINLLMRLTDDYLFISDSQQNALNLIV
QY 892 PEYGCVVNLRKTVN--FPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRILEVQ
Db 839 NNGEFMNDQKITTNFQPOEDYNL---EHPKISVQNECQWIGKSIDMNTLEIK
QY 950 ARTSIRASLTFRNGFKAGNRMRKLFGLVRLKCHSLFLDL-----QVNSLQTI
Db 893 KQTQOEINQTNVAISI-KNLKSLQKNKLR---SLFLNQLIDYFNPNINSFEG
QY 1003 ---KILLQAYRFHACVLQL-----PFHQQVMK---NPTFLRVISDTAS---
Db 948 HHSKATVMKFPFMTKLFQIDLKKSQYSVQYQKENTNENFLKDILYYTVEDVCI
QY 1045 -----SILKAKNAGMSLGAAGAAGPLPSEAVQW
Db 1008 QFEDEINSNIKEIFKNLYSWIMWDIIVSYLKKKKQ-----FKGYLNKL-----
QY 1078 FLLKLTRHRVTYVPL-LGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTLI
Db 1051 -LQIRKSRFFYLKEGCKSLQLILSQYQYQNLNKELEAIEFIDLNNLIQDIKTLI

RESULT 6
S53396
telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8543.12, protein YLR318w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-No
C;Accession: S53396

[illegible]

human herpesvirus 4 (strain B95-8)
herpesvirus 4, Epstein-Barr virus
985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
742

Deininger, P.L.; Farrell, P.J.; Barrell, B.G.

1, 21-45, 1983
e analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
er: A93065; MUID:85035713; PMID:6092825
742

DNA

Q <BAN>

ier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
211, 1984
uence and expression of the B95-8 Epstein-Barr virus genome.

er: A03794; MUID:84270667; PMID:6087149
lation; protein coding region
sequence contains four perfect repeats (residues 149-273, 274-398, 399-521)

2.9%; Score 172.5; DB 1; Length 660;

ilarity 26.1%; Pred. No. 0.00064;

Conservative 16; Mismatches 159; Indels 91; Gaps 16;

QVC--GPLYQLGAATQA--RPPPHASGPERRLGCERAWNSVREAGVPLGLPAPGAR 222
| | | : | | | | | | | | | | | |
QRCAPGPPTRSAAAAQTTHRRPPGCCPSARNPGCPRTWR---RRSGAQRGHPPPGAG 300

3GSARSLP - LPKRPRRGAPEP - ERTVQGSWAHPGRTGRGFCV - VSPAR -- 277
PSGPTGGRPAAPGAPGTAAAPGPGGGAAPSGATPHPERGSGPADPAAARLPPEQE 360

-----PAEET\$LEGAL-----S\$TRHSHP 297

LPQDLAAQRCPCGPPFTRSGAAAQTHRRPPGCPFRSARNPGCPRTWRRRSGAQRGHP 420

```

QY 298 SVGRQHHAGPPSTSRPPRW--DTPCPP-----VYAETKHFLYSSGDKE--
      |           |           |           |           |           |
DQ 421 PPAGQRPSPGTTGRRPAAPGAPGTPAAPGPGGGAAPVSGATPHPERGSGPADPI
      |           |           |           |           |           |
QY 343 PSFLLSSLRPSLTGARRLVETIFLGSRPWMPG-----TPRRLLRLDQ-----
      |           |           |           |           |           |
DQ 481 PERQEPRLPDQLAAAQRCF----AGPPPTTRSGAAAQOQTHRRPPGCFPSARNPG
      |           |           |           |           |           |
QY 390 RLFLLELLGNHAQCPYGVLLKTHCPL--RAAVTPAAGVCAREKPGQSVAAPEEI
      |           |           |           |           |           |
DQ 537 RS-----GAQRGHPPGAGQRPSPGTTGRRPAAPGAPGTPAAPGPGGGAAPVSGI

```

RESULT 9

A59295
 unconventional myosin-15 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-S
 C;Accession: A59295
 R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.
 an, T.B.; Fridell, R.A.
 Genomics 61, 243-258, 1999
 A;Title: Characterization of the human and mouse unconventional myos
 A;Reference number: A59266; MUID:20021762; PMID:10552926
 A;Accession: A59295
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-3511 <LIA>
 A;Cross-references: GB:AF144095; NID:g6224684; PIDN:AAF05904.1; PID:
 C;Genetics:
 A;Gene: MGI:Myo15
 A;Cross-references: MGI:1261811
 A;Map position: 11:33.9
 C;Superfamily: myosin motor domain homology
 F;1209-1871/Domain: myosin motor domain homology <MMO>

Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.59;
Matches 189; Conservative 117; Mismatches 385; Indels 380;

| | | |
|----|-----|---|
| QY | 3 | RAPRCRAVRSLLRSHVREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCCLV |
| Db | 677 | RPPLASPYGSLRQH-----PPW-----AAPAHV |
| QY | 60 | --WDARPPAA-----PSFRQVSLKELVARVLQRLCERGAKNV |
| Db | 708 | NWVGFAEPPGTSPEVAPDLLAFVPRPSFR-----ASRSRSRR |
| QY | 103 | LLDGARGGPPPEAFTTSVRSYLPNTVTD--ALRGSGAWGLLLRRVGDVLLVHLLA |
| Db | 752 | -----SPSLIGSRRRPHLPSPQPSLRSLPGQG----- |
| QY | 161 | LVAPSCAYQVCGPPPLYQLGAATQARPPPHASGPRRRRLGCERAWNHSVREAGVEL |
| Db | 779 | -----YHSPILGPLSPQLSLRRGPFPQPPPPPPRRRQPSLREAF--SLRRASGRL |
| QY | 216 | -----LPAPGARRRGGSASRSILPKR-----PRRGAAPPERT---- |
| Db | 831 | VLGSPRPPSPPLLKHPRHRSNLPSRLPRTWRRLSEPPTRAVKPVWVHRAVPP |
| QY | 256 | WAHPGRTRGPSDRGFCVVSAPAAEATSLEGALSGTRHSHPSVGRQHHAGPPSP |
| Db | 891 | W---GASTGALE-----QQENQREAESETPTWTPPLAPSNDVDMPP |
| QY | 316 | PWDTPC-----PPVYAETKHFLYSS-----GDKEQLRI |
| Db | 936 | PWPEGIGSLRGFSRPPVPVENPILLEHTSPSCPEQSEDVRSNLTGIFLGQHHDGIGI |
| QY | 349 | SLRPSLTGARRLVETIFLGRPWMGTGTPRRRL-PRLPQRYWQMRPLFLELLGNH-- |
| Db | 996 | SADPSL---EKPEEVTTLGD-PQPPAEPEALNTPPNKNVSVSERKVLRLSASYPI |

AQCP-----YGVLLKTHCPLRAAVTPAAGVCAREKPOGS-----434
ATWQWHRWKTVSRTTAPLAPTRAPGPLLKAGEQPAEGRFAVMPQVRGVSSFRPK 1111
--VAAPBEEDTDPRR-----LVQLLRQHSSPWQVYGFVRAC 468
APVQPEHPDQDPEQGPAPQACSLRWPCLPPTDAHCLMSRIRTYSSQSHLRGHGGDC 1171
RL---VPPGLWGSRHNRERFLRNTKFKFISLKGKAKLSLQBLTWKMSVRDCAWLRRSPG 525
SLWKKTRPQSW---QNKMHSTIRNLPMSRREQHRDGVDMTQLEDLQETTVLAN---1225
CVPAAEHRLREEILAKFL-----HWLMSVYVVELLRSF-----FYVT 564
-----LKTRFERNLITYIGSILVSVNPMYRMFAIYGEQVQYSGRALGENPPHLEAIA 1279
TFQK-----NRLFFYR-----KSVWSKL-----QSIGIROHLKRVQLRELSE 603
AFAKMLDAKQNCQVVIISGSGSGKTEATKILRLCLAMNQRRDVMQIQIKILEATPLLE 1339
-----EVRQHREARPAALLTSRLRIFPKPDGLRPIVNMVYVVGARTFRREKRAER-----653
3NAKTVRNDNSSR---FGKFEVIFLEGVIGCAITSQYLLEKSRIVFOAKNERNYHIF 1396
-----LTSRVKALFSVLNVE-----RARRPGLLGASVLGLDDIHRAWRTFVLVRQAQD 701
LLAGLPAQLRQAFSLQEAETYYLNOGNCCEIAGKS--DADDFR-----1441
PELYFVKVDVTGAYDTIPQDRLTEVIAIIPQNTYCVRRYAVVQKAAHGHVRKAFKS 761
-----LLAAMEVLG--FTSEDQDSIFRILASILHGNVYFEKHETDAQEA-----1485
STLTDLQPYMRQFVAHLQETSP--LRDAVVEIQSSSINEASSGLFDVFLRFMCHHAVR 819
VSAREIOA-----VAELLQVSPGLQKAITFKVTETIRE-----KIFTEPLTVESAVD 1534
KSYVQCQGIPOGSIILSTLLCSLCYGDMMENKLFAGI--RRDGLLLRLVD 868
-----DAIAKLYALLFGWLITRVNALVSPKQDTLSIAILD 1572

ein KIAA0522 - human (fragment)
apiens (man)
999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
180
ikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
ion of the coding sequences of unidentified human genes. IX. The complet
ar: Z14086; MUID:98290545; PMID:9628581
180
nary; translated from GB/EMBL/DBJ
mRNA
50 <NAG>
s: EMBL:AB011094; NID:G30433567; PIDN:BAA25448.1; PID:G30433568
urce: brain; clone HG1393

2.4%; Score 142.5; DB 2; Length 1560;
larity 29.5%; Pred. No. 0.25;
Conservative 15; Mismatches 89; Indels 51; Gaps 12;
YQLGAATQARPPPHASGPRRLGCRANWHSVREAGVP-----LGLPAPGARRRG 226
PQLGSI-----PPPPASAP--PVGPFR--HFHAHGPVPGPHYTLGRPGRAPRRGAG 1415
RSLPLPKRP--RRGAAPERTPVQGSWAHPGRTGRGSDRGFCVVSVPARPAEATSL 285
QFAPHGRHPLHQPTSLPLYSPAPQHPPAH---KQGPKHFFIFSHFPQMPAAGAAG 1472
L-SGTRHSHPSVGRQHHAGPPSTSR---PPRPWDTPCPPVVAETKHF-----331

Db 1473 PGRPPFGGSYSHP-----HHPQSPLSPHSPHPSPPLPPSPHTPHSPLPI
Qy 332 LYSSGDKQLRPSFLLSSLRPSLTGARRLVETIFLGSRPW 371
Db 1528 LHASGPPAQTTP--VOTPRPSQA-----GSAPW 1554
RESULT 11
T18314
hypothetical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-C
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandi
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: EMBL:AL034356; NID:el371878; PID:el371559; PIDN:
C:Genetics:
A>Note: L7610.4
Query Match 2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.44;
Matches 111; Conservative 47; Mismatches 195; Indels 121;

Qy 44 PAAFRALVAQCLVCVPWDARPPPAAPSFQVSCLELVARVLQRLCERGAKNVL
Db 366 PSSLHPQQQPVIVLVP---QRPAPPQQERLPRLYSSTRPAGGSPRGAVQNNI
Qy 104 LDGARGGPPEAFTTSVRS-----YLPNTVTDLRGSGAWGLLLRRVGGDVLVHL
Db 423 EDTSSGASEVTSTRSRTRQVFRAPVTASDIPTGS-PYGAM-----
Qy 159 FVLVAPSCAYQVCGPPLYQLGAATQARPPPHASG-----PRRLGC-----
Db 466 YAVVMPQ--RSLPAPPKTGASASAGLPPPSAPAEAAQOPQNSRCPSPSSSRPS
Qy 205 HSVREAGVPLGLPAPGAR-----RRGSASRSLP---LPKRP--RRGAA
Db 524 HAAREQ--PLPQPPPKRPPALPQHQPORAETAKSQLPPRMRLPADPFYSEELI
Qy 250 PVQGSWAHPGTRGSDR-GFCVVSPARPA-----EEATSLGALSGRHSHP
Db 581 ---EGAWDGNASTQSGHGRGHSVRVPSQQQLSLSHEEDLSLSAMLSATVAAP
Qy 303 HHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKQLRPSFLLSSLRPSLTG
Db 638 PYAGHTAPDGEPRPLHVPMPPIIQRP---YAATEE-----G
Qy 362 ETIFLGSRPWMPGTPLRLPRLPQRYWQMRPLFLELLGNHAQCPYG---VLLKTHC
Db 679 RKVTAPQRESDAPSPRHSP-----PAHTLLHSRGAADAGEAAAKETREI
Qy 419 ----VTPAAGVCAREKPKQ-----GSVAAPPEEDTDPRLVQ---LLRQHSSP
Db 729 EAVTAMTTAGVQSSKKPQQLQHEPDGS---PNGDDVD--ELLEADDLIMQPSRP

RESULT 12
EDBEIF
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Fi
C:Species: suid herpesvirus 1
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-F
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713

DNA
60 <CHE>
herpesvirus immediate-early protein IE175
binding; early protein; transcription regulation
2.3%; Score 140; DB 1; Length 1460;
ilarity 24.3%; Pred. No. 0.33;
Conservative 35; Mismatches 163; Indels 158; Gaps 27;
RALVAQCLVCPWDARPPAAPSPFRQVSKLKLVAQLQRCERGAKNVLAFFGALLD 105
RGVLERLLPC-PLRLPAPARAPALGPACLEEVTAALL-----ALRD 746
RG-GPPE-----AFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLAR 155
PGAGPAERQQAADSVLVARIVAPLVYSVDGARAREAAW-----TYA 791
LFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRLGCEAWNH-----S 206
LF---APA---NVAGARL---AEEAARPGAEAP-----GLPPLWPEQGLVVPAPA 837
EAGVPLGLPAPG-----ARRRGGASRSLLPLPKRPRRGAPEPERTPVGGSWAHFGRT 262
AAGAPGLPGSGPSPASTKSGSTKSSGTSGLSGSS-----GYARLPERR 887
PSDRGFCWSP-----ARP---ABEATSLEG-ALSGTRHSHPSVGRQHHAGPPSTSRP-- 313
PSARAAQEEAPRAGARRPGDGEDEGLSGSALRGDGHGRD--DEEDRGPRRKRSLG 945
PRPWTCPPPVYAETHKFLYSSGDKQLRPSFLLSSLRPSLTGARRLVETIFLSRPW 371
PAP--DPAPALVSSSS--SSSEDDRLR-----RP-----LGPMP 980
GTPRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP-----L 415
APDGGFRVPAG-----ETHTPRPSAALAAAYCPPEVARALVDQEVFPPELM 1028
AVT--PA--AGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQV 461
ALTFDPAALAHIAAR---RGAAGAP-----LRRRAAWRQIADPEDV 1069

ATP-binding protein - Deinococcus radiodurans (strain R1)
coccus radiodurans
999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
311
en, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Venter, J.C.; Fraser, C.M.
1-1577, 1999
sequence of the radioresistant bacterium Deinococcus radiodurans R1.
ar: A75250; MUID:20036896; PMID:10567266
311
inary
DNA
2 <WHI>
as: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11688.1; PID:g645993
ource: strain R1
1
2.3%; Score 139.5; DB 2; Length 552;
ilarity 22.3%; Pred. No. 0.094;
Conservative 38; Mismatches 196; Indels 233; Gaps 27;
SGAWGLLLRRVGGDDVLVHLLARCALFVLVAP-----SCAYQVCGP 173
S---RLQFRVSGKSTRIFTSTESLFCLLAPLGLTIASSTGFSFIHSSDVAAATAPRP 80
---LYQLGAATQARPPPHASGPRRLG-----C 199

Db 81 PGTTRHRRGAG--AAPPPFADGPARRGAAAGGAERRRRQNHAAAAARRASCARE
QY 200 ERAWNHVSREAGVPLGLPAPGARRRGGASRSLLPKRPRRGAAPERTPVGC
Db 139 ARRTGSAFRRAGA--AYPERGGAGRRGVLSHSLRGTDARRAAGRGGRTPAAV
QY 260 GRTRGPSDRGFCVVSAPARPAEATSEALSGTTHSHPSVGRQHAGPPSTSRF
Db 195 -RTTRPVGRG-----DYTDRRGALAGARLSHPLA-----RAAPPGDAGE
QY 320 PCPPVYAETHKFLYSSGDKQLRPSFLLSSLRPSLTGARRLVETIFLSRPPMMP
Db 233 -----RPDARAA-----F
QY 380 PRLPQRYWQMRPLFLEL--LGNH-----AQCPYGVLLKTHCPLR
Db 247 HRWPERSGPRRPRRRRAAPGPGCGHGVGAGDPPARGSPDAELAHGVRSGRRTER
QY 423 -----AGVCAREKPGQSVAAPEEEDTD-----PRLVQLLRQHSSPWQV
Db 307 RSPRYSGGASTGTLCTAALVELTDAEVFRNGHRALGPLSWTWAAGQH---WLV
QY 465 VRACLRLRLVP-----PGLWGSRRHNRRLNTKFIISLGKHAKLSLOELTWKMSV
Db 364 GKSTLARLIAGELHPLAGGS--VARPFL-----A
QY 520 LRRSPGVGCVPAEHRILREEILAKFLHWMVSVVVELLSRFFVTE-----TTF
Db 397 RRTTGT---LVSAEVGIRQSGVSGREWLG---DVITASAFAGTEGTDVTA
QY 575 FYRKSVMWSKLQSIGIR-----QHLKRVQLRELSEAEVQRHREARPALI
Db 446 -----WDAVGTLAERDELGELLSDVDVQALSQGLRLLRLARAAVHR-PRLLLL
QY 624 I 624
Db 499 V 499

RESULT 14
S27923
gene LF3 protein - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-J
C;Accession: S27923
R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.
submitted to the EMBL Data Library, August 1990
A;Description: Sequence and transcription of Raji Epstein-Barr virus
A;Reference number: S27923
A;Accession: S27923
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <PAR>
A;Cross-references: EMBL:M35547; NID:g330420; PIDN:AAA45896.1; PID:g
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxy
Query Match
Best Local Similarity 27.0%; Pred. No. 0.23;
Matches 80; Conservative 25; Mismatches 136; Indels 55;
QY 179 GAATQARP-----PPHAGSPRRRLGCCERAWNHVSREAGV-----PLGLPAPGAR
Db 26 GAADPADPVGHPPAAPRAPGPEPRTLQPA---TPRRSGAADPADPVGHPPA--AP
QY 229 SRSLPLPKRPRRGAAPERTPVGGQSWAHGPRTRGSPDRGFCVVSAPARPAEEA
Db 81 PRTRLQPATPRRSGAADP-ADPVG-----HPAAPRAPGPEPRTRLQPATPRRSG
QY 289 LSGTRHSHPSVGRQHAGP-----PSTSR-----PPRPWDTCPPPVYAETHKFI
Db 135 PVG-----HPAAPRAPGPEPRTRLQPATPRRSGAADPADPVGHPPA--P-----

11:43:37 2004

us-09-424-686f-2.rpr

[illegible]

```

ate receptor chain NMDAR2D-1 - rat
; norvegicus (Norway rat)
999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
219
yoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
8, 2836-2843, 1993
ur characterization of the family of the N-methyl-D-aspartate receptor
r: A45219; MUID:93155102; PMID:8428958
219
nary; not compared with conceptual translation
mRNA
;6 <ISH>
urce: brain
extracted from NCB1 backbone (NCBIP:124264)
methyl-D-aspartate receptor 2D; glutamate receptor homology
glutamate receptor homology <GRH>

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2.3%; Score 135; DB 1; Length 1356;
 larity 27.2%; Pred. No. 0.67;
 Conservative 16; Mismatches 102; Indels 118; Gaps 22;

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'ARPPAA-----PSFRQVSLKELVARVLQRLCERGAKNVLAFGFALLDG----- 106
| | | | |
'APPPCAYLDLEPS-----PSDSEDSGLGGASLGLELPWFEA 1124
```

---ARGGPPEAFTTSVRSYLPNTVTDALRG--SGAWGLLLRRVGDDVLVHLARCA 157
| | | | | : | | | |
YPYAERLGPPPGGRYSV-----DKLGGWRAGSDWLYPPRGGP--AWHCHCA 1172

LVAP-----SCAYQVC-----GPLYQLGAATQARPPPHASGP---RRRLGCERAWN 204
| : | | :: || || || || || || || || || || || || || || || || || ||
LLPPPRHLSCSHDGLDGWWAPP-----PFWAAGPPPPRRRARCGRCPHP 1221

REA-GVPLGLPAGARR--GG-----SASRL-PLPKRPRRGAAPEPT-PVG 252
+ : | | | | | | | | | | | | | | | | | |
RASHRAPAAAPHHRHRRRAAGGWDFPPAPTSSLEDLSSRP----CP-PHRTGDTG 1276

WAHPGRTRGPDRCFVWSP-----ARPAEATSLLEGALSGTRHSHPSVGRQHH 305
||| || | :|| ||| ||| :|| ||
WAHAGALR-----ISPAPSPRYDAAPPTTPAAPSUSA---GHGPFRGAUKWT 1324

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'STSR-----PPR--PWTPCPP 323
      :         |         |         |
WVGKDRNGPGRTFFGAASCAP 1348
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April 22, 2004, 00:17:19

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ein search, using sw model

April 21, 2004, 21:01:06 ; Search time 22 Seconds
(without alignments)
2679.246 Million cell updates/sec

JS-09-424-686F-2
1961
MPRAPRCRAVRSLLRSHYRE.....TALEAANPALPSDFKTILD 1132

LOSUM62

lapop 10.0 , Gapext 0.5

41681 seqs, 52070155 residues

its satisfying chosen parameters: 141681

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

| Query | Match | Length | DB | ID | Description |
|-------|-------|--------|------------|--------|--------------|
| 00.0 | 1132 | 1 | TERT_HUMAN | O14746 | homo sapien |
| 58.8 | 1122 | 1 | TERT_MOUSE | O70372 | mus musculus |
| 10.0 | 988 | 1 | TERT_SCHPO | O13339 | schizosacch |
| 7.5 | 1031 | 1 | TERT_EUPAE | O00939 | euplotes ae |
| 6.6 | 1132 | 1 | TERT_OXYTR | O76332 | oxytricha t |
| 6.1 | 1117 | 1 | TERT_TERTH | O77448 | tetrahymena |
| 6.0 | 884 | 1 | TERT_YEAST | O06163 | saccharomyc |
| 3.0 | 3530 | 1 | MY15_HUMAN | P9ukn7 | homo sapien |
| 2.9 | 660 | 1 | YHL1_EBV | P03181 | epstein-bar |
| 2.5 | 653 | 1 | SF01_MOUSE | Q64213 | mus musculus |
| 2.5 | 1003 | 1 | MBD6_HUMAN | Q96dn6 | homo sapien |
| 2.4 | 3511 | 1 | MY15_MOUSE | Q9qzz4 | mus musculus |
| 2.4 | 1461 | 1 | IE18_PRVIF | P11675 | pseudorabie |
| 2.3 | 997 | 1 | IF2_BORPE | Q7vyr2 | bordetella |
| 2.2 | 623 | 1 | DTX1_XENLA | Q8aw93 | xenopus lae |
| 2.2 | 946 | 1 | IP3L_HUMAN | P27987 | homo sapien |
| 2.2 | 1185 | 1 | DRPL_HUMAN | P54259 | homo sapien |
| 2.2 | 657 | 1 | DEND_HUMAN | O94850 | homo sapien |
| 2.2 | 888 | 1 | SM6B_HUMAN | Q9h3t3 | homo sapien |
| 2.2 | 1446 | 1 | IE18_PVKKA | P33479 | pseudorabie |
| 2.2 | 621 | 1 | VP40_HSVBC | P54817 | bovine herp |
| 2.2 | 2716 | 1 | OSA_DROME | Q8in94 | drosophila |
| 2.2 | 709 | 1 | ANDR_RABIT | P10357 | turnip yell |
| 2.2 | 628 | 1 | V70K_TYMV | Q63627 | rattus norv |
| 2.1 | 1048 | 1 | SRA4_RAT | Q8iwy9 | homo sapien |
| 2.1 | 1226 | 1 | CDN1_HUMAN | Q95107 | bos taurus |
| 2.1 | 505 | 1 | WASL_BOVIN | Q7whg2 | bordetella |
| 2.1 | 997 | 1 | IF2_BORBR | Q9nyz3 | homo sapien |
| 2.1 | 720 | 1 | GTSE_HUMAN | P08392 | herpes simp |
| 2.1 | 1298 | 1 | ICP4_HSV11 | O43516 | homo sapien |
| 2.1 | 503 | 1 | WAIP_HUMAN | P50617 | rattus norv |
| 2.1 | 653 | 1 | DEND_RAT | P09951 | rattus norv |
| 2.1 | 704 | 1 | SYNI_RAT | | |

| | | | | | | | |
|----|-------|-----|------|---|------------|--------|----|
| 34 | 123 | 2.1 | 646 | 1 | VP40_HSVEB | P28936 | eq |
| 35 | 123 | 2.1 | 916 | 1 | RTJK_DROME | P21328 | dr |
| 36 | 123 | 2.1 | 960 | 1 | SM6C_RAT | Q9wt13 | ra |
| 37 | 122.5 | 2.1 | 276 | 1 | PRPL_HUMAN | P10162 | ho |
| 38 | 122.5 | 2.1 | 1083 | 1 | T2D3_HUMAN | O00268 | ho |
| 39 | 122 | 2.0 | 872 | 1 | IP3L_RAT | P42335 | ra |
| 40 | 122 | 2.0 | 1522 | 1 | ARHB_HUMAN | O15085 | ho |
| 41 | 122 | 2.0 | 2715 | 1 | MLL4_HUMAN | Q9umh6 | ho |
| 42 | 121.5 | 2.0 | 234 | 1 | PRPM_HUMAN | P10161 | ho |
| 43 | 121.5 | 2.0 | 620 | 1 | EXTN_TOBAC | P13983 | ni |
| 44 | 121.5 | 2.0 | 942 | 1 | M3KE_MOUSE | Q9wul6 | mu |
| 45 | 121.5 | 2.0 | 1321 | 1 | IRS2_MOUSE | P81122 | mu |

ALIGNMENTS

RESULT 1
TERT_HUMAN
ID TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catal;
DE subunit) (HEST2).
GN TERT OR TRT OR EST2 OR TCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews
RA Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and h
RL Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton B.N., Ellisen L.W., Steiner P.,
RA Caddie S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu
RA Bacchetti S., Haber D.A., Weinberg R.A.;
RT "hEST2, the putative human telomerase catalytic subunit gene, is
RT regulated in tumor cells and during immortalization.";
RL Cell 90:785-795(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene
RT encoding the human telomerase reverse transcriptase (hTERT).";
RL Gene 232:97-106(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a temp
CC sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Interacts with PINK1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: Activation of telomerase has been implicated in cel
CC immortalization and cancer cell pathogenesis.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.

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email to license@isb-sib.ch).

350; AAC51672.1; -.
 167; AAC51724.1; -.
 394; AAD30037.1; -.
 393; AAD30037.1; JOINED.
 585; AAG23289.1; -.
 ; T03844.
 ; 11730; TERT.

596; C:telomere; TAS.
121; F:telomeric template RNA reverse transcriptas. . .; TAS.
3R000477; RVTse.

3:R003545; Telomerase RT.

78; rvt; 1.

1365; TELOMERASERT.

: RNA-directed DNA polymerase; Telomere; Nuclear protein;

516 516 D -> G (IN REF. 2).
132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

100.0%; Score 5961; DB 1; Length 1132;

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-arity 100.0%; Pred. No. 0;

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Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRCRAVRSLLRSHYREVLPLATFVRRRLPGQWRLVQRGDPAAFRALVQCLVCVPW 60

APRCRAVRSLLRSHYREVLPLATFVRRRLPGQWRLVQRGDPAAFRALVQCLVCVPW 60

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{PPAAPSFQVSCLKELVARVLQRLCERGAKNVLAFGFALLDARGSPPEAFTTSVR   120  
|||  
|||  
|||  
|||  
{PPAAPSFQVSCLKELVARVLQRLCERGAKNVLAFGFALLDARGSPPEAFTTSVR   120
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.PNTVTDALRSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGA 180

.PNTVTDALRSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGA 180

)ARPPPHASGPRRLGCBRAWNHVSVEAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
 |||||
)ARPPPHASGPRRLGCBRAWNHVSVEAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
 |||||

PEPERTVVGQGSWAHPGTRGPSDRGFCVSPARPAEEATSELGALSGTRHSHPSVG 300
PEPERTVVGQGSWAHPGTRGPSDRGFCVSPARPAEEATSELGALSGTRHSHPSVG 300

HAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEOLRPSFLSSLRPSLTGARRL 360
 |||||
 HAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEOLRPSFLSSLRPSLTGARRL 360

'IFLGSRPMPGTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

GVCAREKPGSGVAAPPEEEDTDPRLVLQLLROHSSPWQVYCFVRACLRRLLVPPGLWGS 480
 |||||
 GVCAREKPGSGVAAPPEEEDTDPRLVLQLLROHSSPWQVYCFVRACLRRLLVPPGLWGS 480
 |||||
 GVCAREKPGSGVAAPPEEEDTDPRLVLQLLROHSSPWQVYCFVRACLRRLLVPPGLWGS 480
 |||||

ERRFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540

FLHNLMSVYVVELLRSFFYVTTTFQKNRLFFYRKSVMYKLSIGIRQHLKRVQLRE 600

AEVROHREARPALITSRRLFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660

| | | | |
|----|------|--|--|
| QY | 661 | LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVT | |
| Db | 661 | LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVT | |
| QY | 721 | PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMR | |
| Db | 721 | PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMR | |
| QY | 781 | QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGPQG | |
| Db | 781 | QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGPQG | |
| QY | 841 | LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPDY | |
| Db | 841 | LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPDY | |
| QY | 901 | RKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSYARTSI | |
| Db | 901 | RKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSYARTSI | |
| QY | 961 | NRGFKAGRNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHA | |
| Db | 961 | NRGFKAGRNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHA | |
| QY | 1021 | FHQQVWKNPTFFLRVISDTSALCYSLKAKNAGMSLGAKGAAGPLPSEAVQWLCI | |
| Db | 1021 | FHQQVWKNPTFFLRVISDTSALCYSLKAKNAGMSLGAKGAAGPLPSEAVQWLCI | |
| QY | 1081 | KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKILTD | |
| Db | 1081 | KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKILTD | |

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RESULT 2
TERT_MOUSE
ID TERT_MOUSE STANDARD; PRT; 1122 AA.
AC 070372; O35432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase cataly
DE subunit).
GN TERT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=9582020;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., Depinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during
RT development, differentiation and proliferation.";
RL Oncogene 16:1723-1730(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393668; PubMed=9724727;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
RT "Expression of mouse telomerase catalytic subunit in embryos and
RT adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
RN [3]
RP SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of Mus musculus telomerase catalytic subunit
RT homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a temp
CC sequence within the RNA component of the enzyme.

```

Interacts with PINX1 (By similarity).
LAR LOCATION: Nuclear.
TY: Belongs to the reverse transcriptase family.
use subfamily.

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: Bioinformatics Institute. There are no restrictions on its
: profit institutions as long as its content is in no way
: this statement is not removed. Usage by and for commercial
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:mail to license@isb-sib.ch).

11; AAC09323.1; -
11; AAC34821.1; -
35; AAB84200.1; -
2709; Tert.
R000477; RVTse.
R003545; Telomerase_RT.
8; rvt; 1.
365; TELOMERASERT.
RNA-directed DNA polymerase; Telomere; Nuclear protein;

553 553 I -> V (IN REF. 3).
122 AA; 127977 MW; F85266905DD6558C CRC64;

58.8%; Score 3505; DB 1; Length 1122;
larity 62.4%; Pred. No. 7.8e-216;
Conservative 122; Mismatches 260; Indels 52; Gaps 13;

APRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLRQGDPAAFRALVAQCLVCPW 60
APRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLRQGDPAAFRALVAQCLVCPW 60

PPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFGFALLDARGGPPEAFTTSVR 120
PPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFGFALLDARGGPPEAFTTSVR 120

PNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
PNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180

ARPPPHAS-GPRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGSASRS 231
ARPPPHAS-GPRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGSASRS 231

WPSVSAVSRPTRPVGRNFTNLRLFLQIKSSSRQEAQKPLALPSRGTKRHLSTSTS 240
WPSVSAVSRPTRPVGRNFTNLRLFLQIKSSSRQEAQKPLALPSRGTKRHLSTSTS 240

PKRPRRGAAPERTPVQSGWAHPGRTGRPSDRGFCVVSAPAR-----PAEATSLE 286
PKRPRRGAAPERTPVQSGWAHPGRTGRPSDRGFCVVSAPAR-----PAEATSLE 286

AKKARCYVPRVEGP-----HRQVLPSPGKSW-VPSPARSPVPTAEKDLSSK 292
AKKARCYVPRVEGP-----HRQVLPSPGKSW-VPSPARSPVPTAEKDLSSK 292

SGTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPVPVYAEKHFYSSGD-KEQLRPSF 345
SGTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPVPVYAEKHFYSSGD-KEQLRPSF 345

SDLSLS-GSVCKHKPSSTSLSPRQNAFQLRP-FIETRHFLYSRGDQGERLNPSF 350
SDLSLS-GSVCKHKPSSTSLSPRQNAFQLRP-FIETRHFLYSRGDQGERLNPSF 350

SLRPSLTGARRLVETIFLGSPPWPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405
SLRPSLTGARRLVETIFLGSPPWPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

NLQPNLTGARRLVETIFLGSPPWPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPY 410
NLQPNLTGARRLVETIFLGSPPWPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPY 410

LKTHCPPLRAA---VTPAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462
LKTHCPPLRAA---VTPAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

LRSHCRFRATANQQVTDAL-----NTSPPHLMDLLRLHSSPWQVY 452
LRSHCRFRATANQQVTDAL-----NTSPPHLMDLLRLHSSPWQVY 452

643 RTFRREKRAERLTSRVKALFSLVLYNERARRPGLLGASVLGLDDIHRWRTFVLR
643 RTFRREKRAERLTSRVKALFSLVLYNERARRPGLLGASVLGLDDIHRWRTFVLR

633 RALGRRKQAQHTQRLKTLFSLMLNERTKHPHLMGSSVGLMNDIYRTWRAFLVLR
633 RALGRRKQAQHTQRLKTLFSLMLNERTKHPHLMGSSVGLMNDIYRTWRAFLVLR

703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVQKAAHGHV
703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVQKAAHGHV

693 TPRMYFVKADVTGAYDAIPQGLVEVVMIRHSESTYCIQYAVVRDSQGVV
693 TPRMYFVKADVTGAYDAIPQGLVEVVMIRHSESTYCIQYAVVRDSQGVV

762 HVSTLTLQPYMRQFVAHLQET--SPLRDVAVVIEQSSSLNEASSGLFVFLRFM
762 HVSTLTLQPYMRQFVAHLQET--SPLRDVAVVIEQSSSLNEASSGLFVFLRFM

753 QVTTLSDLQPYMGQFLKHLQDSASALRNSVIEQSISSNESSSLFDFFLHFL
753 QVTTLSDLQPYMGQFLKHLQDSASALRNSVIEQSISSNESSSLFDFFLHFL

820 IRGKSYVQCQGIPOGSIILSTLLCSLCYCDMENKLFAGIRRDGLLLRLVDDFLV
820 IRGKSYVQCQGIPOGSIILSTLLCSLCYCDMENKLFAGIRRDGLLLRLVDDFLV

813 IGDRCYTQCQGIPOGSIILSTLLCSLCYCDMENKLFAGIRRDGLLLRLVDDFLV
813 IGDRCYTQCQGIPOGSIILSTLLCSLCYCDMENKLFAGIRRDGLLLRLVDDFLV

880 AKTEFLTLVGVPEYGCVVNLKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLI
880 AKTEFLTLVGVPEYGCVVNLKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLI

873 AKTEFLTLVGVPEYGCVVNLKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLI
873 AKTEFLTLVGVPEYGCVVNLKTVVNFVPEDEALGGTAFVQMPAHGLFPWCGLI

940 LEVQSDYSSYARTSIRASLTFRNGFKAGRMRRKLFGLRLKCHSLFLDLQVNSI
940 LEVQSDYSSYARTSIRASLTFRNGFKAGRMRRKLFGLRLKCHSLFLDLQVNSI

933 LEVQSDYSSYARTSIRASLTFRNGFKAGRMRRKLFGLRLKCHSLFLDLQVNSI
933 LEVQSDYSSYARTSIRASLTFRNGFKAGRMRRKLFGLRLKCHSLFLDLQVNSI

1000 NIYKILLQAYRFHACVLPQPHQVWKNPTFFLRVISDTASILCYSLKAKNAG
1000 NIYKILLQAYRFHACVLPQPHQVWKNPTFFLRVISDTASILCYSLKAKNAG

993 NIYKILLQAYRFHACVLPQPHQVWKNPTFFLRVISDTASILCYSLKAKNAG
993 NIYKILLQAYRFHACVLPQPHQVWKNPTFFLRVISDTASILCYSLKAKNAG

1060 GAAGPLPSEAVQWLCHQAFLLKLRHRTVYVPLGLSLRTAQTLQSLRKLPGTTLTY
1060 GAAGPLPSEAVQWLCHQAFLLKLRHRTVYVPLGLSLRTAQTLQSLRKLPGTTLTY

1053 GS---FPPEAAHWCYQAFLLKLAHSAVYIKCLLGLPLRTAQTLQSLRKLPGTTLTY
1053 GS---FPPEAAHWCYQAFLLKLAHSAVYIKCLLGLPLRTAQTLQSLRKLPGTTLTY

1120 NPALPSDFKTILD 1132
1120 NPALPSDFKTILD 1132

1110 DPALSTDFQTILD 1122
1110 DPALSTDFQTILD 1122

RESULT 3
TERT_SCHPO
ID TERT_SCHPO STANDARD; PRT; 988 AA.
AC O13339; O13338;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase cataly
DE subunit).
GN TRT1 OR SPBC29A3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews
RA Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and hu
RL Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels
RA James K., Jones L., Jones M., Leather S., McLean J., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.

940;
M N.A.
4210; PubMed=9110970;
Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
nscriptase motifs in the catalytic subunit of
561-567(1997).
Telomerase is a ribonucleoprotein enzyme essential for
lication of chromosome termini in most eukaryotes. It
s telomeres. It is a reverse transcriptase that adds
sequence repeats to chromosome ends by copying a template
within the RNA component of the enzyme.
LAR LOCATION: Nuclear.
TY: Belongs to the reverse transcriptase family.
se subfamily.
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mail to license@isb-sib.ch).
AAC47515.1; -.
R000477; RVTse.
R003545; Telomerase_RT.
8; rvt; 1.
365; TELOMERASERT.
RNA-directed DNA polymerase; Telomere; Nuclear protein;
031 AA; 122562 MW; 57B87A63A1FED60F CRC64;
larity 7.5%; Score 448.5; DB 1; Length 1031;
larity 22.2%; Pred. No. 6.3e-21;
Conservative 125; Mismatches 303; Indels 57; Gaps 16;
ACLRRLVPPGLWGRHNRRLNRTKFKISLGHAKLSLQELTWKMSVRDCAWLRSS 523
EFFYNILPKDFTGR-NRKNFQKKVKYVELNKHLEIHNKLLLEKINTREISWQVE 419
GCVPAAEHRLREELAKFLHLMVSVVVELLRSEFFYVTTTFQKNRLLFFYRKSVWSK 583
KHFFYFDHE-NIYVLWKLRFEDLVVSLRCCFFYVTEQQSKSYKTYRKNINWV 478
IGIRQHLKRVQLRELSEAEVRQHRARPALLTSRLRFPKPDGLRPVNNMDYVVGAR 643
MSIAD-LKKETLAEVQKEVEEWKSL-GFAPGKLRLLPKTTFRPIMTFN-----KK 532
REKRAERLTSRVKALFSLNVERARR---PGLLGASVGLDDIHRAWRTFVLVRAQ 700
SDRKTTLTNTKLNLSHMLKTLKNRMFKDPFGFAVNYDDVMKYEFEVCKWK-Q 591
PELYFVKVDVTGAYDTIPQDRLTEVI-----ASIIKPQNTYCVRRYAV 746
PKLFFATMDIEKCYDSVNRKLSFLTKTKLLSSDFWMTAQILKRKNIVIDSKNF 651
AAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSLRDADVIEQSSSLNEASSGLF 806
EMKDYFRQFKQK-IALEGGQYPTLFSVLENEQNDLNKAKTLIVEAKQRYFKDNL 710
LRFMCHHAVIRGKSVYQCGIPIQSGISLSTLLCSLCYGDMEKLFAGIRRD----- 860
INICQYNYINFNGKFYKQTKGIPQGLCVSSILSPFYATLEESSLGLRDESMNPEN 770
GLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNLRTKTVNFPVEDEALGGT 917
VLLMRLTDDYLLITTOENNAVLFIKLNINVRNGFKFNMKLQTSFPLSPSKPAKY 830
JMPAHGLF----PWCGLLDTRTLLEVQSDYSSYARTSIRASLTEN-RGFKAGNMRR 972
831 GMDSEVEQNIQDYCDWIGISIDMKTLALMPNINLRIE-GILCTLNLMQTKKA
973 KLFGLVRLKCHSLFLDLQVNSLQTVCT-----NIYKILLQAYRFHACVLQLP
890 KLXSFMLMNNITHYF-----RKTITTEFANKTLNKLFISSGKYKMQCAKEYK
1027 KNPTFFELRVISDTASLCYSILKA 1049
941 KNLAMSSMIDLEVSIIYSVTRA 963
RESULT 5
TERT OXYTR
ID TERT OXYTR STANDARD; PRT; 1132 AA.
AC O76332;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catal;
DE subunit) (Telomerase subunit P133).
GN TERT.
OS Oxytricha trifallax (Sterkiella histriomuscorum).
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Sterkiella.
OX NCBI_TaxID=94289;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337940; PubMed=9671703;
RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
RT "Telomerase reverse transcriptase genes identified in Tetrahymen
RT thermophila and Oxytricha trifallax."
RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a tem
CC sequence within the RNA component of the enzyme.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.

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CC -----
CC EMBL; AF060230; AAC39163.1; -.
DR PIR; T31107; T31107.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW Transferase; RNA-directed DNA polymerase; Telomere; Nuclear prot
KW DNA-binding.
SQ SEQUENCE 1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
Query Match 6.6%; Score 395; DB 1; Length 1132;
Best Local Similarity 22.2%; Pred. No. 1.8e-17;
Matches 136; Conservative 114; Mismatches 305; Indels 58;
OY 450 QLLRQHSSPWQYGVFVRACLRRLVPPGLWGRHNRRLNRTKFKISLGHAKLS
DB 451 QLFYQQDQRQISNFLTTEFVANVPKPFLECK-NKKIFNKKMLQFVKFNRFESFT
OY 510 WKMSVRDCAWLRSPGVGCVPAAEH---RLREELAKFLHLMVSVVVELLRSPF
DB 510 NKFRVNEVSWL-----SFKCKDENKKFFMNEHVFVKLVKWFEDLAILMRCYF
OY 567 TFQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQLRELSEAEVRQHRARPALLTSRL
DB 566 AKEYQRIFYTRKNINWMIMRLSIDDLLKQ-NLKQVEKKEMRIFCESQ-NFAPGKL

[illegible]

STANDARD; PRT; 1117 AA.

(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
nucleotidyl transferase subunit P133).

thermophila.
alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
ia; Tetrahymena.
;911;

M. N. A.

17940; PubMed=9671703;
Sparger J.M., Chapman K.B., Cech T.R.;
reverse transcriptase genes identified in Tetrahymena
and Oxytricha trifallax";
Acad. Sci. U.S.A. 95:8479-8484 (1998).

M. N. A.

17941; PubMed=9671704;

transcriptase component of the Tetrahymena telomerase protein complex.";

Acad. Sci. U.S.A. 95:8485-8490(1998).

1: Telomerase is a ribonucleoprotein enzyme essential for replication of chromosome termini in most eukaryotes. It is telomeres. It is a reverse transcriptase that adds sequence repeats to chromosome ends by copying a template within the RNA component of the enzyme.

ILAR LOCATION: Nuclear.

TY: Belongs to the reverse transcriptase family.

use subfamily.

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CC or send an email to license@isb-sib.ch).

| | |
|----|----------------------------------|
| DR | EMBL; AF062652; AAC39135.1; -. |
| DR | EMBL; AF061284; AAC39140.1; -. |
| DR | PIR; T14891; T14891. |
| DR | InterPro; IPR000477; RVTse. |
| DR | InterPro; IPR003545; Telomerases |
| DR | Pfam; PF00078; rvt; 2. |
| DR | PRINTS; PR01365; TELOMERASERT. |
| KW | Transferase; RNA-directed DNA |
| KW | DNA-binding. |
| SQ | SEQUENCE 1117 AA; 133317 MW |

Query Match 6.1%; Score 363; DB 1; Length 1117;
Best Local Similarity 20.2%; Pred. No. 2e-15;
Matches 193; Conservative 160; Mismatches 368; Indels 234;

```

322 PPVYAETKTHFLYSSGDKQEQLRPSFLSLRPSITGARRLLVETIFLGRSPWMPGT.
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
239 PGVF-KSSFFNYS-----EIKKGFOFKVIOEKLGRQ-----FINSDKIKPDH
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
382 --LPQRY-----WQMRPLFLE---LLGNHAQCPYGVLLKTHCPLRAAVTPAI
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
287 KTLKEYOSKNFSCOEERDLFLEFTEKIVONFNFNFNFVLLKKFKCL-----
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

| | | |
|----|-----|---|
| Qy | 429 | EKPQGSVAAPEEEDTDPRRLVQLLRQHS-----SPWQVYGI |
| | | : : : : : |
| Db | 334 | -----PENYCSLKSOVKOIVOSENKAAOOSCENLSLYDTEISYKQITNI |

QY 470 RRLVPPGLWGSRHNERRRFLRNTKKFISLGKHAKLSQLLTWKMSVRDCAWLRSI
:
D6 385 QNCVPNQLGKG-NEKVLEKLYEFVOMRFENOKVLDDYICFMDFDVWF----

QY 530 PAAEHL-----REILAKFLHLMMSVVVVELLRSSFYVTETTFQKRLFI!
:
dP 436 DLKNOKFTOKKYISDKRKILGDLIVFIINKTIVIPWRYNFYITEKHKEGSOLF
: :|| : ::| : || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
:

QY 581 W---SKLQSIGI-RQH LKRVQLRELSEAEVQRHREARPALTSRLRFIPKP DGLI
| | | | : : : : : : : : : : : :
db 496 WKLVSKI.TTVIKLEENI.EKVFEKI.I PEDSECKVPD-----SKLPIDKVGSTF

QY 637 DYVGARTFREKRAERLTSRVKALFS-----VLNYERARRPGLLGASVLGLDDII

QY 693 FVLVRQAQPPPELYFVKVDVTGAYDTIPDRLTEVIASIIKPONTYCVRRYAV
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 600 FIEKWKNG-EPOLVAAU.DIKKKCVDSIDOMKI.I.NEENOSN.IODTVETNKVII

```

QY      753  GHVRKAFKSHVSTLTDLQ-----PYM-----RQFVAHLQE-----
                                     |||
Db      659  DLILOIOCTNNINSAMETFEFFYINKYDFWMNINDEPVVNIKEPQIAYGIVDNNY
                                     |||

```

OY 783 ---TSPLRDAWVIEQSSSLNEASSGLEDFVLRFMCHHAVIRKGSYYVOQGIPQ
 :| | :| | :| | :| | :| | :| | :| | :| | :| |
NH 219 EYEIQSNDDDELIVNODKPDCSTVDIYNTH KHTGCAUT CENVTNGTCAGTICPIS

[illegible]

QY 892 PEYGCVVNLRKTVVN--FPVEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVQSE
 830 NNNGCEMENDVQVTTMTTQFQDQDQVNT FUKYKICVNTQCGYKICVATFQVYKIFVZ

[illegible]

(Rel. 40, Last sequence update)
(Rel. 43, Last annotation update)
Inconventional myosin-15).
O15.
; (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
1762; PubMed=10552926;
ng A., Belyantseva I.A., Anderson D.W., Probst F.J.,
Miller W., Touchman J.W., Jin L., Sullivan S.L.,
Camper S.A., Lloyd R.V., Kachar B., Friedman T.B.,
; ation of the human and mouse unconventional myosin XV
sible for hereditary deafness DFNB3 and Shaker 2.";
243-258(1999).

ENCE FROM N.A., AND VARIANTS DFNB3 TYR-2111 AND PHE-2113.
7311; PubMed=9603736;
ng Y., Fridell R.A., Probst F.J., Wilcox E.R., Camper S.A.,
., Morton C.C., Morell R.J., Noben-Trauth K., Camper S.A.,
; of unconventional myosin MYO15 mutations with human
; deafness DFNB3.";
1447-1451(1998).
; Myosins are actin-based motor molecules with ATPase
; Unconventional myosins serve in intracellular movements.
ghly divergent tails are presumed to bind to membranous
ents, which would be moved relative to actin filaments (By
ty). May play a role in the formation or maintenance of
n-rich structures of the inner ear sensory hair cells.
LAR LOCATION: Cytoplasmic.
PECIFICITY: Highly expressed in pituitary. Also expressed
levels in adult brain, kidney, liver, lung, pancreas,
and skeletal muscle. Not expressed in brain. In the
y, highly expressed in anterior gland cells.
Defects in MYO15A are the cause of autosomal recessive
omic deafness type 3 (DFNB3) [MIM:600316].
TY: Contains 1 myosin-like globular head domain.
TY: Contains 1 FERM domain.
TY: Contains 3 IQ domains.
TY: Contains 1 MYTH4 domain.
TY: Contains 1 SH3 domain.

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94; AAF05903.1; -
76; -; NOT_ANNOTATED_CDS.
A59266.
; 1BR2.
7594; MYO15A.
-
05; P:hearing; TAS.
R000299; Band_4.1.
R000448; IQ_region.
R001609; myosin_head.
R000857; MYTH4.
R001452; SH3.
2; IQ; 3.
3; myosin head; 1.
4; MYTH4_2.
193; MYOSINHEAVY.
0355; myosin_head; 1.
95; B41; 1.

DR SMART; SM00015; IQ; 3.
DR SMART; SM00242; MYSC; 1.
DR SMART; SM00139; MYTH4; 2.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS00096; IQ; 3.
DR PROSITE; PS00002; SH3; FALSE_NEG.
KW Myosin; ATP-binding; Actin-binding; Coiled coil; Repeat; SH3 don
KW Calmodulin-binding; Disease mutation; Deafness.
FT DOMAIN 1 1887 MYOSIN HEAD-LIKE.
FT DOMAIN 1888 2029 NECK OR REGULATORY DOMAIN.
FT DOMAIN 2030 3530 TAIL.
FT DOMAIN 1323 1350 COILED COIL (POTENTIAL).
FT DOMAIN 1792 1799 ACTIN-BINDING (POTENTIAL).
FT DOMAIN 1902 1924 IQ 1.
FT DOMAIN 1925 1954 IQ 2.
FT DOMAIN 1955 1976 IQ 3.
FT DOMAIN 2867 2953 SH3.
FT DOMAIN 3209 3530 FERM.
FT NP_BIND 1315 1322 ATP (POTENTIAL).
FT VARIANT 2111 2111 N -> Y (in DFNB3; family from Bengk
/FTId=VAR_010303.
FT VARIANT 2113 2113 I -> F (in DFNB3; Indian family).
/FTId=VAR_010304.
SQ SEQUENCE 3530 AA; 395171 MW; 3D103923D4BCBE4A CRC64;

Query Match 3.0%; Score 176.5; DB 1; Length 3530;
Best Local Similarity 20.6%; Pred. No. 0.0068;
Matches 263; Conservative 144; Mismatches 392; Indels 475;

QY 107 ARGGPPEAFTTS-----VRSYLP-----NTVTDALRC
Db 2313 SRGGPKVVFNGSWDSDEDMSTRPQOEHPKVLDSGYSSHNDGTNGETEQRG
QY 139 LLRRVGGDDVLVHLLARCALFVLVAP-----SCAYQVCGPPLYQLGA
Db 2372 QESDSLGEPAVPHKGLDCYLDLSLFDPLVLSYGDADLEKPTAIAYRMKGGQPGGGG
QY 182 -TQARPP---PHASGPRRLGRCERAWNHVSREAGV---PLGLPAPGARRRGGAS
Db 2432 DTPRRPPEPKPIPLDASTLALQAFIH--KQAVLLARGMTLQATALQQQLSAA
QY 234 LPKRRRGAAPERTPVGGQSWAHGRTGRGSPDRGFCVWSPARPAEEATSLEGA
Db 2490 AEKPP---APEAQPTSVGTGPPAKPVLLR-----ATPKPLAPA-----
QY 294 HSHPSVGRQHAGPPSTSRPPRPWDTPCPVVA-----ETKFLYSSGDKBQLR
Db 2525 -----PLAKAPRLPIKPVAAAPVLAQDQASPET-----TSPSPELVR
QY 348 SSLRPSLTGARRLVETIFLGSRPMPGTPRRLPRLPQRYWQMRP-----LFLE
Db 2566 SEHFPOPT--QQIKNIVRQYQQPFRGGRPEALRKDGKVFMRKRPDPHEEALMLLK
QY 401 AQCPYG-----VLLK--THCPLRAAVTPAAGVCAREKPGQGSVAAPEE-EDTD
Db 2624 LAAAPGTQVSREAVALKPVTSAP-RPSMAPTSAL-----PSRLEPPELTQTR
QY 450 --QLLRQHSSPWQVYGFVR-----ACLR--
Db 2678 NPNFYGYQDAPWKI--FLRKEVFYPKDSYSHVPQLDLLFRQILHDTLSEACLRIS
QY 473 VPPGLWGSRRHNERFLRNTKKFISLG-KHAKLSLQELTWKMSVRDCAWLRSPGV
Db 2736 RMKALFAQNQ-----LDTQKPLVTESVKRAVVSTARDTWEV-----YFSRIFPAT
QY 532 AEHRLREEILAKFLHLMVSVVVELLR-----SFFVYTETTF
Db 2786 G-----VQLLA-----VSHVGIKLLRMVKGQEGAGQLRVLAYSFADILEFTM
QY 573 LFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQRHREARPAULTSLRFLPKP.

NLAS--EKVILFSARAH---QVKTLDVDFILELKK----- 2867
MDYVVGARTFRREKRAELTSRVKALFVINYERA-----RRPGLLGAS----- 679
SDYVAVVAVNLPEDPA-----LLAFHKGDIIHLQPLEPPRVGVSGACVVR 2913
TGLDDIHR-----AWRTFVLVRVRAQPPPELYFVKVDVTGAVD-----TIP-QDRLT 726
VYLEELRRRGPDGFWRGFTIHGRVGRPPSEL-----VQPAAPDFLQLPTEPGRGAA 2969
ASIIKQNTYCVRRY-----AVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQ 781
AAVASAAAAQEVGRRREGPPVRRARSADHGEDALALPPY-TMLEFAQKYFRDPQRRPQ 3028
-----TSPLRDAVVEIQSSSLNEASSGLDFVFLRFMCHHAVR 819
RLKSKEPRESRTLEDMLCFTKTPLESLSIELSDSLSKMATDMLAVMRFMGDAPLK 3088
KSYVQCQGIPOGSIILSTLLCSLCYGD---MENKLFAGI-----RRDG 861
DLDVLCN-----LLKLC-GDHEVMRDECYQVVKQITDNTSSKQDSCQGW 3136
RLVDDF---LLVTPHLTHAKTFLRLVR---GVPEYG---CVNLRKTVVFPVED 911
YIVTAHSCSEVHLPHLTR---FLQDVSRTPGLPFGQIAKACEQNLOKTL----- 3186
GGTAFVQMPAHGLFPWCGLLLDTRTLEEVQSDYSSYARTSTRASLTFRNGFKAGRNMR 971
GG-----RLPLPSS-----IELRAML-----AGRSSK 3210
F-----GV---LRLKCHSLFLDLQVNSLQTVCT-----NIYKILLQAYRFA 1014
FLPLGGLERHLKIKTCTVALDV---VEEICAEMALTRPEAFNEYVIFVVTNRGQHV 3266
-----QLPFHQVQWKNPTFF-----LRVISDTASLCY 1044
SRRAYILDVASEMEQVDGGYMLWFRVRLWDQLKFENELYVTMHNQVLPDYLGKLF 3326
KAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLLKLTRHRTV---YVPLLGSLRTAQ- 1100
PASR-----PSEQ---LLQOVSKLASLQHRADKDHFLP---SVREVQE 3366
TQLSRKLPGETT 1111
AQLYRTTAGST 3380

STANDARD; PRT; 660 AA.

(Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 36, Last annotation update)
BHLF1 protein.
virus (strain B95-8) (Human herpesvirus 4).
NA viruses, no RNA stage; Herpesviridae;
irinae; Lymphocryptovirus.
0377;

M.N.A.
0667; PubMed=6087149;
kier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Barrell B.G.;
a and expression of the B95-8 Epstein-Barr virus genome.";
07-211(1984).

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DR EMBL; V01555; -; NOT_ANNOTATED_CDS.

DR PIR; A03742; Q0BE3.

KW Hypothetical protein; Early protein; Repeat.

FT DOMAIN 149 648 4 X 125 AA TANDEM REPEATS.

FT REPEAT 149 273 1.

FT REPEAT 274 398 2.

FT REPEAT 399 523 3.

FT REPEAT 524 648 4.

SQ SEQUENCE 660 AA; 66244 MW; 86DA1D67A37152A2 CRC64;

Query Match 2.9%; Score 172.5; DB 1; Length 660;

Best Local Similarity 26.1%; Pred. No. 0.0014;

Matches 94; Conservative 16; Mismatches 159; Indels 91;

QY 167 AYQVC--GPPLYQLGAATQA--RPPPHASGPRRRRLGCERAWNHSVREAGVPLGLI

Db 244 AAQRCPPAGPPPTSGAAAOQTHRRPPGCPRSARNPGCPRTWR---RRSGAQRGHI

QY 223 RRGSSASRSLP-LPKRPRRGAPEP-ERTPVQGSWAHPGTRGPDSDRGFCV-V

Db 301 QRESGPTGGRPAAPGAPGTPAAGPGGGAAVPSGATPHPERGSGPADPPAAARLI

QY 278 -----PAEATSLEGAL-----SG

Db 361 PRLPQDLAAQRCPPPTSGAAAOQTHRRPPGCPRSARNPGCPRTWRRRSGI

QY 298 SVGRQHAGPPSTSRPRPW--DTPCPP-----VYAETKFLYSSGDKE---

Db 421 PPGAGQRPSTGGRPAAPGAPGTPAAGPGGGAAVPSGATPHPERGSGPADPP

QY 343 PSFLLSSLRPSLTGARRLVETIFLGRPRMPG-----TPRRLPRLPQ-----

Db 481 PERQEPRLPQDLAAQRCPP-----AGPPPTSGAAAOQTHRRPPGCPRSARNPGCI

QY 390 RPLFLELLGNHAQCPYGVLLKTHCPL--RAAVTPAAGVCAREKPGQSVAAPEEEI

Db 537 RS-----GAQRGHPPPGACQRPSTGGRPAAPGAPGTPAAGPGGGAAVPSGAT

RESULT 10

SF01_MOUSE

ID_SF01_MOUSE STANDARD; PRT; 653 AA.

AC Q642I3; O08817; P70167; Q61454; Q921Z4;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Splicing factor 1 (Zinc finger protein 162) (Transcription facto

DE ZFM1) (mzfm) (Zinc finger gene in MEN1 locus) (Mammalian branch

DE binding protein mBBP) (BBP) (CW17).

GN SF1 OR ZFP162 OR ZFM1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS CW17 AND CW17E).

RC STRAIN=C57BL/10; TISSUE=Spleen;

RX MEDLINE=97355688; PubMed=9212169;

RA Wrehlike C., Schmitt-Wrede H.-P., Qiao Z.D., Wunderlich F.;

RT "Enhanced expression in spleen macrophages of the mouse homolog

RT human putative tumor suppressor gene ZFM1.";

RL DNA Cell Biol. 16:761-767(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/10;

RX MEDLINE=99287587; PubMed=10360842;

RA Wrehlike C., Wiedemeyer W.-R., Schmitt-Wrede H.-P., Mincheva A.,

RA Lichter P., Wunderlich F.;

RT "Genomic organization of mouse gene zfp162 (mzfm).";

TY: Contains 1 myosin-like globular head domain.
TY: Contains 1 FERM domain.
TY: Contains 2 IQ domains.
TY: Contains 1 MYTH4 domain.
TY: Contains 1 SH3 domain.

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mail to license@isb-sib.ch.

95; AAF05904.1; -
30; AAC40124.1; -
10; BAA36582.1; -

A59295.
T42386.

; 1BR2.

1811; Myo15.

R000299; Band_4.1.

R000048; IQ_region.

R001609; myosin_head.

R000857; MYTH4.

R001452; SH3.

2; IQ; 2.

3; myosin_head; 1.

4; MYTH4; 2.

193; MYOSINHEAVY.

0355; myosin_head; 1.

95; B41; 1.

15; IQ; 2.

42; MYSC; 1.

39; MYTH4; 2.

26; SH3; 1.

0096; IQ; 2.

0002; SH3; 1.

0660; FERM_1; FALSE_NEG.

0661; FERM_2; FALSE_NEG.

0057; FERM_3; 1.

binding; Actin-binding; Coiled coil; Repeat; SH3 domain;

tion; Deafness.

1 1871

872 2013 MYOSIN HEAD-LIKE.

014 3511 NECK OR REGULATORY DOMAIN.

307 1334 TAIL.

776 1783 COILED COIL (POTENTIAL).

886 1908 ACTIN-BINDING (POTENTIAL).

909 1938 IQ 1.

848 2934 IQ 2.

190 3511 SH3.

299 1306 FERM.

779 1779 ATP (POTENTIAL).

330 1331 C -> Y (IN SH2).

579 1579 MISSING (IN REF. 2).

955 1972 L -> R (IN REF. 3).

077 2077 MISSING (IN REF. 2).

139 2139 L -> M (IN REF. 2).

953 2953 L -> P (IN REF. 2).

511 AA; 395533 MW; 38C962F98A2D395B CRC64;

larity 2.4%; Score 144; DB 1; Length 3511;

Conservative 117; Mismatches 385; Indels 380; Gaps 44;

RCRAVRSLLRSHYREVLPATFVRLGPGQWRLVQGDPAAFRALVAQCLVCVP--- 59

RLASPYGSLRQH-----PPPW-----AAPAHVFPFPPQA 707

DARPPPPAA-----PSFRQVSCLELVARVLQRLCERGAKNVLAFGFA 102

GFAEPPGTSPEVAPDLLAFVPRPSFR-----ASRSRSRRAAYGFP 751

QY 103 LLDGARGGPPEAFTTSVRSVLPNTVTD--ALRGSGAWGLLLRRVGGDDVLVHLLAI
Db 752 -----SPSLIGSRRRPHLPSPQPSLRSLPQGG-----
QY 161 LVAPSCAYQVCGPPPLYQLGAATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLC
Db 779 -----YHSPGLPLSPQLSLRRGPPFPFPFPPRRRPSQLREAF--SLRRASGRLC
QY 216 -----LPAPGARRRGGSASRSLSPLPKR-----PRGAAPERT---E
Db 831 VLGSPPRPSPPLPKHGPRHRSNLPSRLPRTWRLSEPPTRAVKPWWHAYPPE
QY 256 WAHPGRTRGPSDRGFCVVSPARPAEAEATSLGALSGRHSHSPSVGRQHAGPPST
Db 891 W---GASTGALE-----QQENQREAESETPTWTPPLAPSWDVMPPPT
QY 316 PWDTPC-----PPVYAETKHFLYSS-----GDKEQLRE
Db 936 PWPEGISLRGFSRPPVPENPLLEHTSPSPCEQSEDRVSNLTGIFLGQHDPGF
QY 349 SLRPSLTGARRLVETIFLGRPMPGTPRRL-PRLPQRYWQMRPLFLELLGNH--
Db 996 SADPSL---EKPEEVVTLGD-POPPEAEALNPTPNKNVVSERKVLRLSASYPI
QY 401 --AQCP-----YGVLLKTHCPLRAAVTPAAGVCAREKPGQS-----
Db 1052 ARATWPQWHRWKTVSRTAPAPLAPTRAPGPLLKAGEQRAEPGRFAVMPQVRGVS
QY 435 ----VAPEEEDTDP--LVQLLRQHSSPMQVYV
Db 1112 GPAPVQPPPEHPDQPEQGPAPQACSLRWPCLPWPPTDAHCLWSRIRTYSSQSHLRG
QY 469 LRRLL---VPPGLWGRHNRERFLRNTKKFISLGKHAHLSQELTWKMSVDRCAWL
Db 1172 HKSLWKTKTRPQSW---QNMKHSIRNLPMSRREQHREDGVEDMTQLEDLQETTTL
QY 526 VGCVPAAEHLREEILAKFL-----HMLMSVYVVELLSRF-----
Db 1226 ----LKTRFERNLITYIGSILSVNPNYRMEFAIYGEQVQVQYSGRALGENPPH
QY 565 ETTFQK-----NRLFFYR-----KSVMSKL-----QSIGIRQHLKRVL
Db 1280 NLAFAKMLDAKQNCQVILSGESGSGKTEATKLLRCLAAMNQRDRVMQIKILEA
QY 604 A-----EVQRHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAER
Db 1340 AFGNAKTVRNDSSR---FGKFVEIFLEGVCICAITSQYLLEKSRIVFQAKNER
QY 654 -----LTSRVKALFSLVNYE-----RARRPGLLGASVLGLDDIHRAWRTFVLR
Db 1397 YELLAGLPAQLRQAFSLQEAETYYVNLQNGNCEIAGKS--DADDFRR-----
QY 702 PPPELYFVKVDVTGAYDTIPQDRLTEVIASIKPQNTYCVRRYAVVQKAAHGHVR
Db 1442 -----LLAAMEVLG-FTSEDQDSIFRILASILHGNVYFEKHETDAQEVA-----
QY 762 HVSTLTDLQPYMROFVAHLQETSP--LRDAVVIEQSSSLNEASSGLFDVFLRFMC
Db 1486 SWSAREIQ-----VAELLQVSPEGLQKAITFKVTETIRE-----KIFPLTV
QY 820 IRGKSYVQCQGIQPGSILSTLLCSLCYGMENKLFAGI--RRDGLLRLVD 868
Db 1535 AR-----DAIAKVLVALLFGWLITRVALVSPKQDTLSIALD 157:

RESULT 13
IE18-PRVIF
ID IE18 PRVIF STANDARD; PRT; 1461 AA.
AC P11675;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)

```

arly protein IE180.

3 virus (strain Indiana-Funkhauser / Becker) (PRV).
3 DNA viruses, no RNA stage; Herpesviridae;
3 Virinae; Varicellovirus.
3 1523;

2M N.A.
15207; PubMed=2546124;

ide sequence analysis of the immediate-early gene of
3 virus."
is Res. 17:4637-4646(1989).

OV-1989) to the EMBL/GenBank/DBJ databases.
: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
TING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
RAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
LAR LOCATION: Nucleus of infected cells.
ong stretch of serine residues may be a major site of
ylation.
TY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.

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Bioinformatics Institute. There are no restrictions on its
-profit institutions as long as its content is in no way
this statement is not removed. Usage by and for commercial
quires a license agreement (See http://www.isb-sib.ch/announce/
mail to license@isb-sib.ch).

; CAA33214.1; --
EDBEIF.
R005205; Herpes_ICP4_C.
R005206; Herpes_ICP4_N.
5; Herpes_ICP4_C; 1.
4; Herpes_ICP4_N; 1.
n; Transcription regulation; Trans-acting factor;
Phosphorylation; Nuclear protein.
390 405 POLY-SER.
958 966 POLY-SER.
461 AA; 149833 MW; 7F31E7ABE403B208 CRC64;

2.4%; Score 142; DB 1; Length 1461;
larity 23.9%; Pred.No. 0.35;
Conservative 33; Mismatches 158; Indels 172; Gaps 28;

ALVAQCLVCVPWDARPPPAAPSPRQVSCLKELVARVLQRLCERGAKNVLAFGFALLD 105
:: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3VLERLLPC-PLRLPAPARAPALGPACLEEVTAALL-----ALRD 746

3-GPPE-----AFTTSVRSYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLAR 155
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
3AGPAERQQAADSVALVARTVAPLVRYSDVGARAREAAW-----TYA 791

FVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRRLGCERAWNH-----S 206
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
3----APA---NVAGARL----AEEAARPGPAEPAP---GLPPLMPEQPLVVPAPA 837

AGVPLGLPAPG----ARRRGSASRSLPLPK-----RPRRGAAPERTPV 251
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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3WAHPGRTRGPSDRGFCVVPARP--AEEATSLEG-ALSGTRHSHPSVGRQHAGPP 308
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
---RKKRRAPGAR-----RPGDGEDEGLSGSALRGDGHGRD--DEEDRGPR 938

3P-----PRPWDTPCPVPVAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRLVETI 364
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
3SLGLGPAP--DPAPALVSSSSS--SSSSEDDRRL-----RP----- 974

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GenCore version 5.1.6
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tein search, using sw model

April 21, 2004, 23:41:41 ; Search time 83 Seconds
(without alignments)
4303.212 Million cell updates/sec

US-09-424-686F-2
MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTILD 1132

apop 10.0 , Gapext 0.5

017041 seqs, 315518202 residues

its satisfying chosen parameters: 1017041

ngth: 0
ngth: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- SPTREMBL 25:*
- : sp_archaea:*
- : sp_bacteria:*
- : sp_fungi:*
- : sp_human:*
- : sp_invertebrate:*
- : sp_mammal:*
- : sp_mhc:*
- : sp_organelle:*
- : sp_phage:*
- 0: sp_plant:*
- 1: sp_rodent:*
- 2: sp_virus:*
- 3: sp_vertebrate:*
- 4: sp_unclassified:*
- 5: sp_rvirus:*
- 6: sp_bacteriap:*
- 7: sp_archaeap:*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

| Query | Length | DB | ID | Description |
|-------|--------|----|--------|--------------------|
| 93.7 | 1069 | 4 | Q8NG46 | Q8ng46 homo sapien |
| 68.0 | 807 | 4 | Q8N6C3 | Q8n6c3 homo sapien |
| 66.6 | 795 | 4 | Q8NG38 | Q8ng38 homo sapien |
| 60.9 | 1128 | 11 | Q9QXZ4 | Q9qxz4 mesocricetu |
| 47.4 | 524 | 4 | Q9UBR6 | Q9ubr6 homo sapien |
| 38.9 | 1191 | 13 | Q9DE32 | Q9de32 xenopus lae |
| 37.0 | 523 | 4 | Q94807 | Q94807 homo sapien |
| 33.8 | 575 | 11 | Q9JK99 | Q9jk99 rattus norv |
| 23.0 | 514 | 11 | Q9R266 | Q9r266 mus musculu |
| 12.2 | 1123 | 10 | Q9SE99 | Q9se99 arabidopsis |
| 12.2 | 1123 | 10 | Q9SPU7 | Q9spu7 arabidopsis |
| 11.5 | 1259 | 10 | Q9AU13 | Q9aul3 oryza sativ |
| 11.0 | 1261 | 10 | Q8LKW0 | Q8lkw0 oryza sativ |
| 8.0 | 1032 | 5 | Q7Z1L1 | Q7z1l1 euplotes cr |
| 8.0 | 1032 | 5 | Q8MUB3 | Q8mub3 euplotes cr |
| 7.5 | 85 | 4 | Q9UN56 | Q9uns6 homo sapien |

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|----|-------|-----|------|----|--------|-----------|
| 17 | 449 | 7.5 | 116 | 11 | Q8OSU5 | Q8osu5 r |
| 18 | 441 | 7.4 | 1032 | 5 | Q7Z1L0 | Q7z1l0 eu |
| 19 | 408 | 6.8 | 823 | 5 | Q8SQQ0 | Q8sqq0 en |
| 20 | 397 | 6.7 | 104 | 11 | Q9JLM1 | Q9jlm1 m |
| 21 | 395.5 | 6.6 | 1135 | 5 | Q8I8Z7 | Q8i8z7 st |
| 22 | 394 | 6.6 | 73 | 4 | Q9UNR4 | Q9unr4 ho |
| 23 | 392 | 6.6 | 1108 | 5 | Q8I8Z6 | Q8i8z6 st |
| 24 | 365 | 6.1 | 867 | 3 | Q9P8T3 | Q9p8t3 ca |
| 25 | 364 | 6.1 | 895 | 5 | Q9GRC5 | Q9grc5 pa |
| 26 | 361 | 6.1 | 867 | 3 | Q9P8T2 | Q9p8t2 ca |
| 27 | 342 | 5.7 | 896 | 5 | Q8MUQ8 | Q8muq8 pa |
| 28 | 339 | 5.7 | 79 | 6 | Q7YR69 | Q7yr69 fe |
| 29 | 200 | 3.4 | 52 | 11 | Q9R0B3 | Q9r0b3 m |
| 30 | 188.5 | 3.2 | 960 | 5 | Q9NCP5 | Q9ncp5 gi |
| 31 | 179 | 3.0 | 2675 | 2 | Q9FBZ3 | Q9fbz3 st |
| 32 | 167 | 2.8 | 1474 | 5 | Q962F9 | Q962f9 cr |
| 33 | 161 | 2.7 | 1070 | 4 | Q96JG5 | Q96jg5 ho |
| 34 | 159 | 2.7 | 771 | 10 | Q9XHY4 | Q9xhy4 o |
| 35 | 152.5 | 2.6 | 296 | 12 | Q69118 | Q69118 h |
| 36 | 152 | 2.5 | 1285 | 10 | Q9LWK0 | Q9lwk0 o |
| 37 | 151.5 | 2.5 | 539 | 10 | Q9SR71 | Q9sr71 a |
| 38 | 151.5 | 2.5 | 669 | 4 | Q8N4X0 | Q8n4x0 ho |
| 39 | 150.5 | 2.5 | 653 | 11 | Q08817 | Q08817 m |
| 40 | 150 | 2.5 | 611 | 11 | Q8K0M8 | Q8k0m8 m |
| 41 | 150 | 2.5 | 850 | 11 | Q9JJ15 | Q9jj15 m |
| 42 | 150 | 2.5 | 850 | 11 | Q80XI6 | Q80xi6 m |
| 43 | 148.5 | 2.5 | 1305 | 11 | Q80YF9 | Q80yf9 m |
| 44 | 147.5 | 2.5 | 986 | 12 | Q9DW99 | Q9dw99 r |
| 45 | 147 | 2.5 | 1186 | 12 | Q7T401 | Q7t401 s |

ALIGNMENTS

| | | | | | |
|----------|--|--------|--------------|------|----------|
| RESULT 1 | | | | | |
| Q8NG46 | ID | Q8NG46 | PRELIMINARY; | PRT; | 1069 AA. |
| AC | Q8NG46; | | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Created) | | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Last sequence update) | | | | |
| DT | 01-OCT-2003 (Tremblrel. 25, Last annotation update) | | | | |
| DE | Telomerase reverse transcriptase. | | | | |
| GN | HTERT. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.; | | | | |
| RT | "Exon 11 deleted variant of the human telomerase reverse | | | | |
| RT | transcriptase." | | | | |
| RL | Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AB085628; BAC11010.1; - | | | | |
| DR | GO; GO:0005634; C:nucleus; IEA. | | | | |
| DR | GO; GO:0003677; F:DNA binding; IEA. | | | | |
| DR | GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA. | | | | |
| DR | GO; GO:0003721; F:telomeric template RNA reverse transcriptas. | | | | |
| DR | InterPro; IPR003545; Telomerase_RT. | | | | |
| DR | PRINTS; PR01365; TELOMERASERT. | | | | |
| KW | RNA-directed DNA polymerase. | | | | |
| SQ | SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64; | | | | |
| | Query Match 93.7%; Score 5583.5; DB 4; Length 1069; | | | | |
| | Best Local Similarity 94.4%; Pred. NO. 0; | | | | |
| | Matches 1069; Conservative 0; Mismatches 0; Indels 63; | | | | |
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| Db | 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQGDPAAFRALVAQCL | | | | |
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JVVNFFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOSSYSSYARTSIRASLTF 960
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JQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1017
JRHRTVYVPLLGSLRTAQQLSRKLPGLTTLTALEAAANPALSDFKTILD 1132
JRHRTVYVPLLGSLRTAQQLSRKLPGLTTLTALEAAANPALSDFKTILD 1069

ID Q8N6C3 PRELIMINARY; PRT; 807 AA.
AC Q8N6C3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta and gamma deletion isoform of telomerase reverse transcriptase.
DE HTERI.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach cancer;
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamam
RA Kazumasa H.;
RT "Both beta and gamma deletion isoform of human telomerase rever
RT transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptas.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
SQ SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;

Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.9e-304;
Matches 763; Conservative 0; Mismatches 0; Indels 0;

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Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPPEA
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Db 541 LAKFLHWMMSVYVVELLSRFFYVTTTFFQKNRLFYRKSVWSKLQSIGIRQHHLK
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(TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
variant of telomerase reverse transcriptase.
(Human).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Homnidae; Homo.
606;
M.N.A.
Ch;
Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
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JN-2002) to the EMBL/GenBank/DBJ databases.
50; BAC11015.1; -.
34; C:nucleus; IEA.
77; F:DNA binding; IEA.
64; F:RNA-directed DNA polymerase activity; IEA.
21; F:telomeric template RNA reverse transcriptas...; IEA.
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365; TELOMERASERT.
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arity 98.4%; Pred. No. 2.4e-298;
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QY 721 PQDRLTEVIAIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 711 --DRLTEVIAIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHV 751
RESULT 4
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ID Q9QXZ4 PRELIMINARY; PRT; 1128 AA.
AC Q9QXZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in trans
cells";
RL Biochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptas...
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
Query Match 60.9%; Score 3628; DB 11; Length 1128;
Best Local Similarity 63.3%; Pred. No. 1.9e-271;
Matches 736; Conservative 124; Mismatches 238; Indels 64; C
QY 1 MPRAPCRCAVRSLRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQCLV
Db 1 MPRAPCRCAVRSLRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQCLV
QY 61 DARPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFI
Db 61 DSQPPPADLSFHQVSSLKELVARVQRLCERGERNVLTGFGALLNGAQGGPPMTFI
QY 121 SYLENTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY

PRELIMINARY; PRT; 1191 AA.

(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
reverse transcriptase.

is (African clawed frog).
metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
trachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopus.
1355;

M N.A.
Ishikawa F.;
reverse transcriptase of Xenopus laevis.";
EC-1999) to the EMBL/GenBank/DBJ databases.
199; AAG43537.1; --

34; C:nucleus; IEA.
177; F:DNA binding; IEA.
23; F:RNA binding; IEA.
64; F:RNA-directed DNA polymerase activity; IEA.
21; F:telomeric template RNA reverse transcriptas. . .; IEA.
40; F:transferase activity; IEA.
78; P:RNA dependent DNA replication; IEA.
R000477; RVTse.
R003545; Telomerase_RT.
8; rvt; 2.

365; TELOMERASERT.
DNA polymerase; Transferase.
191 AA; 138016 MW; 98D9D776869A57D6 CRC64;
38.9%; Score 2316.5; DB 13; Length 1191;
larity 42.4%; Pred. No. 5.6e-170;
Conservative 201; Mismatches 381; Indels 123; Gaps 25;

APRCRAVRSLLRSHYREVLPATFVRLG-PQGR--LVQRGDPAAFRALVAQCLVC 57
RTGATLLSILQRLYGVLGIVEYTDLTQVPGGKVPVLLGDSKFRSFVAVELVVC 60

DARPPAAPSFQVSCLEKELVARVLQRLCERGAQNVLAFGFALLDARGGPPPEAFTT 117
3TKPLSPVSLQSTQREVVARVIOICEKKNVLAFGYGLVD-EKNSLNIRLTP 119

SYLPNTVTDALRGSGAWGLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLY- 176
NYFPNPTTTTISTISILWETLLTRVGDDVMYWLQCSIFVFPVPPRCYQITGQPIYT 179

-----QLGAATQAR-----PPPHASGPRRLGCRANWHSVRE 209
DDVFLFQSQSFTQSNVLLRYIKRNVFHLRKKYLPKHSMTSRM-----LTWRNKSP 234

PLGLPAPGARRRGGSASRSL-----PLPKRPRGAPE-----PERTPVGQG 254
JIRSKTSMVTTTEIHSKRKLCSKDICIPIPKKRDNDKDDTVDHFDLPKCRSVSYL 294

IPGR-----TRG-PSDRGFCVSPARPAEATSLEGALSGRH----- 294
YPKTNVQVTGLITSGYKTKTFQCQKPVSCQKKTAFYSVAGDCNLKDNVNKLI 354

3VGRQHHAGPPSTSRPPRPWDTPCPVPVYAEKHFY-SSGDKEQLRPSFLLSLRPS 353
3V-----PTAQR-----LSFSNIFIDFGRTLYLSISYKKGFSFPLNSLDST 401

ARLLVETIFLGS-----RPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPY 405
3QKLVEITIFLSNPLAEQNFQPKRDENCY--KLPRKYWKMPKPHFQELIQNHKFFPY 459

KTHCPLRAAVTPAAGVCAREKPGQSVAAPEED-----TDPRLVQLLRQHSS 457

Db 460 LVYLNKHCVPSSM-----ACSEKR-----SLQKNRIENDGKQLKHFTTKANLLSL
QY 458 PWQVYGFVRACLRRLVPPGLWGSRRHNERFLRNTKKFISL-GKHAKLSLQELTW
Db 512 IWQVYMFVRECLNNVVPDIMWSSHNKCRFFRNVKSFLLFFSGFKISLSLMLW
QY 517 CAWLRRSPGVCVPAAEHRLREILAKFLHLMVSVVVELLRSEFFVYTTTFQK
Db 572 CSWIRLQKSDHFVPASEHLLREKILAKFVFWLMDTYVIQLLKSFYVTTTFQK
QY 577 RKSVMKLSQSIGIRQHLKRVQLRELSAEVRQHREARPAALLTSRLRFPKPDGL
Db 632 RKSVMKLSQSIGIRQHLKRVQLRELSAEVRQHREARPAALLTSRLRFPKPDGL
QY 637 DYVVGARTFR--REKRAERLTSRVKALFSLVNYERARRPGLLGASVLGLDDIHR
Db 692 SSTLSSQSKENQEKIHFSSQIRNLFSVLNRYEWRNCSLIGSSVFGMDDIYK
QY 695 LRV-RAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAIIP--QNTYCVRRYA
Db 752 LDFEKPQVEKLOFYFVKTDVKAYDTIPHSKLDDEVISKVINPANEVYCIIRYA
QY 752 HGVKAKPKSHVSTLTDLQPMRQFVAHLQETSPLRDVAVIEQSSSLNEASSGLI
Db 812 TGRILSKFRHVSELAADVLPNMKQFVSNQEKLLRNTLILVQNLNLSVVKLI
QY 812 FMCHHAVRIRGKSYVQCQIGIPQGSILSTLLCSLCYGMENKLFAGIRRDGLLRI
Db 872 IIRSHILRIKDRYVMQCCGIPQGSMLSTILCSLCYGMENAMLGGIQKNGVLMRI
QY 872 LVTPLHAKTFLRLTVRGVPEYGCNVNLRKTVNFPVED--EALGGTAFVQMP
Db 932 LVTPLHAKTFLRLTVRGVPEYGCNVNLRKTVNFPVED--EALGGTAFVQMP
QY 930 WCGLLDTRTLEQVQSDYSSYARTSIRASLTFRNGFKAGRNMRKLFGLRLKCHE
Db 989 WCGLLDTRTLEQVQSDYSSYARTSIRASLTFRNGFKAGRNMRKLFGLRLKCHE
QY 990 QVNSLQTVCTNIYKILLQAYRPHACVQLQPLPHQVQVKNPTFFELRVIDSTASLCY
Db 1049 KVNSLRTVCINTYKIFLLQAYRPHACVQLQPLPHQVQVKNPTFFELRVIDSTASLCY
QY 1050 KNAGMSLGAAGAAGPLSEAVQWLCHQAFLLKLTFRHRTVYVPLLGSLRTAQOLS
Db 1109 KNKDLTRGYKDVSCQFNFEAVQWLSYQAFLLKLTFRHRTVYVPLLGSLRTAQOLS
QY 1110 TTLTALEAAANPALPSDFKTILD 1132
Db 1169 DTIELLSVTDSSLHKDFSCIMD 1191

RESULT 7
O94807
ID O94807 PRELIMINARY; PRT; 523 AA.
AC O94807;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Telomerase transcriptase (Fragment).
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsudo M.
RA Inoue M.;
RT "Cloning and characterization of human telomerase catarytic subu
RT (hTERT) gene promoter."
RL Cancer Res. 0:0-0(1999).
DR EMBL; AB016767; BAA74724.1; --.

523 523
23 AA; 56555 MW; 8FDE562DDECC93DA CRC64;
larity 37.0%; Score 2207.5; DB 4; Length 523;
Conservative 3; Mismatches 56; Indels 59; Gaps 6;
APRCRAVRSLLRSHYREVLPLATFVRRRLGPGQWRLVQGDPAAFRALVAQCLVCPW 60
APRCRAVRSLLRSHYREVLPLATFVRRRLGPGQWRLVQGDPAAFRALVAQCLVCPW 60
PPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
PPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
PNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYOVCGPPLYQLGA 180
PNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYOVCGPPLYQLGA 180
ARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSPLPKRPRR 240
ARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSPLPKRPRR 240
PEPERTPVGQSWAHPGRTGPGSDRGFCVVSAPARAEATSLEGALSGTRHSHPSVG 300
PEPERTPVGQSWAHPGRTGPGSDRGFCVVSAPARAEATSLEGALSGTRHSHPSVG 300
HAGPPSTSRPPRPWDTPCPVPVYAEKHFVLYSSGDKBQLRPSFLLSSLRPSLTGARRL 360
HAGPPSTSRPPRPWDTPCPVPVYAEKHFVLYSSGDKBQLRPSFLLSSLRPSLTGARRL 360
IFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
IFLGSPPGQGLPAGCPACPSATGKGCPCFWSCLGTRTSAPTG-----CSSRRTAR 414
GVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPPCLM-- 478
--CELRSPPQPVSVP---GRSPRAL-----W-----RPPRRRTQTPVAVCS 450
-----GSRHNERFLRNTKKFISLGKHAKLSLQELTWK 511
STAPLAGVRLRAGLPAPAGAPRPLGLQAQRRRFLRNTKKFISLGKHAKLSLQELTWK 510
RDCAWLRRSP 524
RDCAWLRRSP 523
PRELIMINARY; PRT; 575 AA.
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, last sequence update)
(TrEMBLrel. 25, last annotation update)
atalytic subunit (Fragment).
jicus (Rat).
atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;
N.A.
S., Xu X., Yu H.;
ase catalytic subunit, rTERT.";
AR-2000) to the EMBL/GenBank/DBJ databases.
18; AAF62177.1; -.
34; C:nucleus; IEA.
77; F:DNA binding; IEA.
23; F:RNA binding; IEA.
54; F:RNA-directed DNA polymerase activity; IEA.
21; F:telomeric template RNA reverse transcriptas. . .; IEA.
40; F:transferase activity; IEA.
78; F:RNA dependent DNA replication; IEA.

DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF0078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
Query Match 33.8%; Score 2016; DB 11; Length 575;
Best Local Similarity 67.6%; Pred. No. 3.5e-147;
Matches 391; Conservative 71; Mismatches 110; Indels 6;
QY 558 RSFFYVTETTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRELSEAEVRQHREA
Db 1 RSFFYITESTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRELSEAEVRQHQA
QY 618 TSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKALFSLVLYERARR
Db 61 ICRLRFIPKPNGLRPIVNMVYSYMGTRALGRRKQAQHTQRLKTLFSLMYERTKH
QY 678 ASVLGLDDIHRAMRTFVLVRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTETVIA
Db 121 SSVGLMNDIYRTWRAFLVRVRAQDQTPRMYFVKADVTGAYDAIPQGLVEVYVNM
QY 737 NTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLDQPYMRQFVAHLQET--SPLRDA
Db 181 STYCIQYAVVRRDSQGVVHKSFRQVTTLSLDLPYMGQFLKHLQSDASALRNS
QY 795 SSSLNEASSGLFDVLFMCHHAVIRGKSVYQCGIPQGSILSTLLCSLCYGD
Db 241 SISMNESSSLFDFLHFLRHSVVKIGDRCTQCQGIQGSILSTLLCSLCYGD
QY 855 AGIRRDGLLLRVDDFLLVTPHLTHAKTFLRLVRGVPEYGCVVNLKRTVVPV
Db 301 AEVQDGLLLRVDDFLLVTPHLTHAKTFLRLVRGVPEYGCVVNLKRTVVPV
QY 915 GGTAFAVQMPAHGLFPWCGLLLDTRTLEQVSDYSSYARTSIRASLTENRGFKAGRN
Db 361 GGAAPYQLPAHCLFPWCGLLLDTRTLEQVSDYSSYARTSIRASLTENRGFKAGRN
QY 975 FGVRLKCHSLFLLDQVNSLQVCTNIYKILLQAYRFHACVLQLPFHQQVWKNP
Db 421 LSVRLKCHGLFLLDQVNSLQVCTNIYKILLQAYRFHACVLQLPFHQQVWKNP
QY 1035 VISDTASLCYSILKAKNAGMSLGAAGAPLPSEAVQWLCHQAFLLKLTTRHRTY
Db 481 IISQASCCYAILKVNPGMTLKASGS---PPPEAAHWLCYQAFLLKLAHSHVY
QY 1095 SLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132
Db 538 PLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 575
RESULT 9
Q9R266
ID Q9R266 PRELIMINARY; PRT; 514 AA.
AC Q9R266;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN TERT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144726; PubMed=10022128;
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams
RA Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-M
RT is not functionally equivalent in cellular transformation.";

[illegible]

PRELIMINARY; PRT; 1123 AA.

(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
reverse transcriptase.

El9.190.
thaliana (Mouse-ear cress).
iridiplantae; Streptophyta; Tracheophyta;
a; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
702;

M.N.A.
clumbia;
2974; PubMed=10471830;
lu H., Tamura K., Takahashi H.:
loning and characterization of AtTERT, a telomerase
scriptase homolog in Arabidopsis thaliana.";
57:465-469 (1999).

M. N. A.
amura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
swes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
JG-2000) to the EMBL/GenBank/DBJ databases.

M.N.A.
is sequencing project;
UG-2000) to the EMBL/GenBank/DBJ databases.
54; AAD54777.1; -.
47; CAC01849.1; -.
TS1517.

34; C:nucleus; IEA.
77; F:DNA binding; IEA.
23; F:RNA binding; IEA.
54; F:RNA-directed DNA

54; F: RNA-directed DNA polymerase activity; IEA.

DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptas.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR000215; Serpin.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00284; SERPIN; 1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1123 AA; 130579 MW; 5645B8295817B7F6 CRC64;

Query Match 12.2%; Score 724.5; DB 10; Length 1123;
Best Local Similarity 23.8%; Pred. NO. 7.1e-47;
Matches 294; Conservative 199; Mismatches 511; Indels 233;

| | | |
|----|-----|--|
| QY | 1 | MPRAPRCRAVRSLLRSHRYEVLPLATFV-----RRLGPQGMW----- |
| Db | 1 | MPRKPRIHRVPEILWRLFGNRARNLNDAILPNRNIOPEQCRCRGQGLGCSSSI |
| QY | 39 | VQRGDPAAFRALVAQCLVCVPWDARPPAAPSFQVSCSLKELVARVLQRL--CF |
| Db | 61 | LRSDDPPIHYRKLHRCFV-VLHEQTPLLDFSPTSWWSQREIVERIEMMQSGCI |
| QY | 96 | VLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRSGGAWGULLRRVGGDVLV |
| Db | 118 | VICARYDKYDQ8-----SPILELLT-SSSWFLLKRVGHDVMV |
| QY | 156 | CALFVLVAPSCAYQVCGPPLYQLGAAT-----QARPPPHASGPRRRRLGCERAWN |
| Db | 160 | TSIFLPLLGKKHQVSGPPLCIKHKRTL SVHENKRKRDDNVQPTKRQWLSSAVL |
| QY | 210 | AGVPLGLPAPG---ARRRGGASRSPLPKRPRRGA-----APEPERTPVG |
| Db | 220 | DSATI-TPIVGEDVDQHREKTKTKRSRIYLKRRRKQKRVNFKKVDNAPCITP-- |
| QY | 258 | HPGRTRGPSDRGFCVSWPARPAERATSLGALSCTRHSHPSVGRQHHAAGPPSTSR |
| Db | 272 | ---STNGKVSTG-----NDENMLHIGINGSLTDFVKQAKQ----- |
| QY | 318 | DTPCPPVYAETKHFLYS-SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPW |
| Db | 304 | -----VKRNKNFKGLSETYSVIPPNHILKTLRPNCSDSKLLMNHIFGEVNVW |
| QY | 377 | RRLPRLPQ---RYWQMRLFIELLGNHAQCPYGVLLKTHCP-----LRAAV |
| Db | 357 | HGKGNCPGSGICLYHSLLSKLKMLGKTKSSHLMLLDKHCPVLLLOEDALKSGT |
| QY | 425 | VCAREK-----PQGSVAA-----PEEEDTPRRVLQLLRQHSSPWQVYGFVRACLR |
| Db | 417 | --RRQKADKLPHGSSSSQTGPKPCPSVEERKL-----YCTNDQVVSFIWAICRY |
| QY | 477 | LWGRHNRERRFLRNTKCFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPA |
| Db | 469 | LLGTHQMRVLRKNIAWFSVRRRNEKCTVNOQLHFKVKPSPDPPFFARKE--LCCMV |
| QY | 537 | REE-----ILAKFLHMLMSVYVVELLRSFFVYTETTFQKNRLFFYRKSVWSK |
| Db | 527 | QSESTSTQMLCTKWISWMLFLEIVKLVHFNFYATESQGGRLNIYYRKRSWER |
| QY | 589 | IRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPVNM DYVVGAR |
| Db | 587 | ISKALDGYVLVDDAEAESSRKK-----LSKEFFLPKANGVRMVL----- |
| QY | 649 | KRAERLTSRVKALFVSLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPP |
| Db | 631 | SRSQSL-----RDTHAVLKDIOQLKEPDVLGSSVFEDHDDFYRNLCPYLIHLRSQSGE |
| QY | 708 | FVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVERYAVWQKAAHGH-----VRJ |
| Db | 687 | FVADVFKAFDSVDQGLLHVIOQSLKDE--YIIINCRVLCCGKRSSWNVNKTIIVS |

NIYQAFLLCAMKEH-CYIRSVSDANVSK--LELLQVIKRTRFYMHSLIVRRMQDVEL 1186
GAAGPLPSEAVQWLCHQAF--LLKLTRHRVTVYVPLLSRLTAQTQLSRKLPQTTLTA 1114
-----HYNVRPVLKLRKRTIWLGLTAYIRVLQOKOSRYKDMLTLLT 1228
1116
1230
PRELIMINARY; PRT; 1032 AA.
(TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
reverse transcriptase.
ssus.
Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
Euplotidae; Moneuplotes.
936;
M.N.A.
Z., Wang L., Shrode T., Bednenko J., Hurley L.A.,
ally programmed gene elimination in Euplotes crassus
a switch in the telomerase catalytic subunit.";
003).
43; AAP42278.1; -.
DNA polymerase.
032 AA; 123265 MW; C44E30B6D6D37953 CRC64;
larity 8.0%; Score 478; DB 5; Length 1032;
Conservative 110; Mismatches 276; Indels 76; Gaps 19;
REFLNTKKFISLGKHAHKLQELTWMKSVRDCAWLRRSPGVCVPAAEHRLREE--- 539
SFQSKIKKYVGLNKHHLIHNKLLGLDKLSIKWL----GFKTSKKNYHYFDKENRF 434
KFLHLMMSVYVVELLSFFVYTTTQKNLFFYRKSVWSKLQSIGIRQHLLKRVQLR 599
RILRWIFEDVVVSLIRCFYVTEQKSYSETYYRKNIDIVMKYSIAD-LNRETL 493
SEAEVRQHREARPAALLTSRLRFPKDPGLRPIVNDYVVGARTFRR-----EKRAER 653
KEDVMKWKNELRFA--PGKRLRIPKTTTFRPIM-----TFNKKIVDPEGKTSK 542
RVKALFVSVLYNERARR---PGLLGASVLGLDDIHRARTFVLRVRAQDPPPELYFVK 710
NTKLSYSHLMKLTILKNRMFKDPFGFAVFNDDVMRKYEEFVLRQVD-RPKLYFVT 601
TGAYDTIPQDRLTEVIAS-----IIKPQNTYCVRRYAVVQKAAHGHVR 756
EKCYDSVDREKLSQFLGTQLLSPNFQIIKVQILKRNINVIDSQNFKKKKMRDYFR 661
KSHVSTLTDLQPYMRQFVAHLQETSPLRDVAVIEQSSSLNEASSGLDFVLRFMCHH 816
QK-IALEGDQYPSLFNVLENDQNELNAKTLLENQKRDYKPKKALLDPVIKICRHN 720
IRGKSYVQCQGIPOQSILSTLLCSLCYGDMMENKLFAGIRRDG-----LLRLV 867
FNRKYKQTKGIPQGLCVSSILSSFFYASLEENALGYLRKESMDANDPNITLLMLRT 780
LLVTHLTHAKTFLRLTVRGVPEYGCVVNLKTVVNFVDEALG--GTAfv--QMP 923
LLITKENNAIFIEKILINVSQRNKFKNMQLQTNFPLDPSKLNKYGMASVEDQNI 840
LFWCGLLDTRTLEVQSDYSSYARTSIRASLTFFN-RGFKAGRNMRRKLFVLRKLC 982

Db 841 AHDIYIDWIGISIDMSTLALMPNI-NLRRKGILCTLNMMNQTKKASMWLKRKL--
QY 983 HSLFLLQVNSLQTVCTN-----YKILLQAYRFHACVQLQPFHQVWKNP
Db 892 KSFLMNNITRYFRKTTITNREFSNKTLNKLKIAGAYKYMQCCIEYKDHFKT--NTJ
QY 1036 ISDTASLCYSILKA 1049
Db 950 DKIIICAIYSVTRA 963
RESULT 15
Q8MUB3
ID Q8MUB3 PRELIMINARY; PRT; 1032 AA.
AC Q8MUB3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT-1.
OS Euplotes crassus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotidae; Euplotidae; Moneuplotes.
OX NCBI_TaxID=5936;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang L., Dean S.R., Shippen D.E.;
RT "Oligomerization of the Telomerase Reverse Transcriptase from E.
RT crassus.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528527; AAM95622.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptas.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1032 AA; 122966 MW; 0C401515839801A8 CRC64;
Query Match 8.0%; Score 474; DB 5; Length 1032;
Best Local Similarity 24.8%; Pred. No. 1.5e-27;
Matches 152; Conservative 112; Mismatches 275; Indels 74;
QY 483 NERRFLRNTKKFISLGKHAHKLQELTWMKSVRDCAWLRRSPGVCVPAAEHRLF
Db 379 NRKSFQSKIKKYVGLNKHHLIHNKLLGLDKLSIKWL----GFKTSKKNYHYFI
QY 540 ILAKFLHLMMSVYVVELLSFFVYTTTQKNLFFYRKSVWSKLQSIGIRQHLL
Db 435 VLWRILRWIFEDVVVSLIRCFYVTEQKSYSETYYRKNIDIVMKYSIAD-LA
QY 600 EL-SEAEVRQHREARPAALLTSRLRFPKDPGLRPIVNDYVVGARTFRR-----E
Db 494 EVPKEDVMKWKNELRFA--PGKRLRIPKTTTFRPIM-----TFNKKILDPE
QY 654 LTRSVKALFVSVLYNERARR---PGLLGASVLGLDDIHRARTFVLRVRAQDPPPE
Db 543 MTNTKLSYSHLMKLTILKNRMFKDPFGFAVFNDDVMRKYEEFVLRQVD-RQVGRPK
QY 711 VDVGTAYDTIPQDRL-----TEVIASIIKPQNTYCVRRYAVVQKAAHGHV
Db 602 MDIEKCYDSVDREKLSQFLGTQLLSPNFQIIKVQILKRNINVIDSQNFKKKKMRDYFR
QY 761 ---SHVSTLTDLQPYMRQFVAHLQETSPLRDVAVIEQSSSLNEASSGLDFVFLRF
Db 662 QKWQKIALEGDQYPSLFNVLENDQNELNAKTLLENQKRDYKPKKALLDPVIKI

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RGKSYVQCQGIPOGSILSTLLCSLCYGDMMENKLFAGIRRDG-----LLRLVD 868
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
NRKYKQTKGIPOGLCVSSILSSFYASLEENALGYLRKESMDANDPNITLLMRLTD 781
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
LVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFVPEDEALG--GTAFV--QMPA 924
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
LITTKENNAILFIEKILINVSQRNKFKNMKKLOTFNPLDP SKLNKYGMASVEDQNIA 841
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
FPWCGLLLDTRTLEVSQDYSYARTSIRASLTEN--RGFKAGNMRRKLFGLVLKXCH 983
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
IDWIGISIDMSTILAMPNI--NLRRKGILCTLNNMQTKKASMWLKRKL-----K 892
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
LDLQVNSLQTVCTN-----IYKILLQAYRFHACVLQLPFHQOVWKNPTFFLRVI 1036
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
MNNITHYFRKTTITNREFSNKTLNKLVIAGAYKYMCCIEYKDHFT--NTEIHPQLD 950
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
ASLCYSILKA 1049
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
CAILYSVTRA 963
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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